

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 36.9123 Seconds  
(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-1  
Perfect score: 2732  
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Xgapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Delopt 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database : Issued\_Patents\_AA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	264	9.7	3878	4	US-09-914-259-111
3	253.5	9.3	2733	4	US-09-949-016-11433
4	253.5	9.3	3259	4	US-09-949-016-6507
5	246.5	9.0	1581	4	US-09-866-108A-15754
6	244	8.9	1960	4	US-09-949-016-10872
7	243	8.9	1960	4	US-09-538-092-1077
8	242	8.9	2663	4	US-09-538-092-1252
9	240.5	8.8	1976	4	US-09-538-092-1078
10	239.5	8.8	2662	4	US-09-595-684B-31
11	238.5	8.7	1695	4	US-09-866-108A-15753
12	238.5	8.7	1780	4	US-09-949-016-6899

13	238.5	8.7	1786	4	US-09-949-016-7880	Sequence 7880, Ap
14	237	8.7	1055	4	US-09-949-016-9776	Sequence 9776, Ap
15	237	8.7	1937	4	US-09-538-092-918	Sequence 918, App
16	235	8.6	994	4	US-09-949-016-6779	Sequence 6779, Ap
17	235	8.6	1972	4	US-08-875-435B-4	Sequence 4, App11
18	234.5	8.6	1939	4	US-09-949-016-6925	Sequence 6925, Ap
19	234.5	8.6	1942	4	US-09-949-016-8135	Sequence 8135, Ap
20	233.5	8.5	631	4	US-08-477-831C-11	Sequence 11, App1
21	233.5	8.5	1935	4	US-09-538-092-916	Sequence 916, App
22	233.5	8.5	1944	4	US-09-949-016-10929	Sequence 10929, A
23	233	8.5	1959	4	US-09-949-016-8134	Sequence 8134, Ap
24	232.5	8.5	976	3	US-09-104-324B-4	Sequence 4, App11
25	232.5	8.5	976	4	US-09-538-092-1339	Sequence 1339, Ap
26	232.5	8.5	1087	4	US-09-914-259-12	Sequence 12, App1
27	232.5	8.5	1939	4	US-09-538-092-915	Sequence 915, App
28	232.5	8.5	1939	4	US-09-949-016-11104	Sequence 11104, A
29	232.5	8.5	2482	1	US-08-328-254-6	Sequence 6, App11
30	232	8.5	606	4	US-08-477-831C-2	Sequence 2, App11
31	232	8.5	1938	4	US-09-949-016-6417	Sequence 6417, Ap
32	232	8.5	1972	4	US-08-875-435B-3	Sequence 3, App11
33	232	8.5	2954	4	US-09-150-867-1	Sequence 1, App11
34	231.5	8.5	2125	4	US-09-919-172-29	Sequence 29, App1
35	231.5	8.5	2704	4	US-09-538-092-1260	Sequence 1260, Ap
36	231.5	8.5	3210	4	US-09-538-092-1154	Sequence 1154, Ap
37	230.5	8.4	1939	3	US-09-310-187A-1	Sequence 1, App11
38	230.5	8.4	1939	3	US-09-538-092-917	Sequence 917, App
39	230	8.4	1427	4	US-09-538-092-1044	Sequence 1044, Ap
40	229.5	8.4	977	4	US-09-010-147B-18	Sequence 18, App1
41	229.5	8.4	1940	4	US-09-538-092-901	Sequence 901, App
42	229.5	8.4	1963	4	US-09-949-016-8888	Sequence 8888, App
43	228	8.3	2310	4	US-09-874-923-120	Sequence 120, App
44	227.5	8.3	2349	4	US-09-538-092-914	Sequence 914, App
45	227.5	8.3	3248	1	US-08-353-700-1	Sequence 1, App11

## ALIGNMENTS

RESULT 1  
US-09-621-976-5141  
; Sequence 5141, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J. B.  
; APPLICANT: Jobert, S.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621, 976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5141  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-621-976-5141

## Alignment Scores:

Pred. No.: 7.75e-20 Length: 62  
Score: 300.00 Matches: 59  
Percent Similarity: 98.33% Conservative: 0  
Best local Similarity: 98.33% Mismatches: 0  
Query Match: 10.98% Indels: 1  
DB: 4 Gaps: 0

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Cy 1138 CAGCTCTCAGCAGCAGCAAGCAAGCTTCTCTGAGAGGCGCAGCCCTGTGCGAAGAGTG 1197  
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Db      21 GlnLeuLeuSerLySGlnAenGlnLeuLeuGlnLurGlnSer--CysArgLySerArgTr 40
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Db      40 pthrgLyCySGLyProSerLyThrAlaCySHisAenLeuLeuAlaAspLeuSerGly 59

RESULT 2
US-09-914-259-11
; Sequence 11, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Les
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3878
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-914-259-11

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DB:              4          Gaps:      22

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Qy      148 CTTCGGCTGCTAAIACCTTGAACCGTGTGTGGTCTTTGTTGAATGTCTCAGCAT 207
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Db      1882 LeuHisGlnLysLeuArgAlaArgGln-----GlnLeuAlaValGlnLeuSerLysAla 1899
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Qy      208 GAAGCTGTCTTCTCCCAACCCATACATATGTCATATGCAAGCATGCAAGACTGGT 267
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Qy      268 AAAGAAAGATGATGATGATGCTGACATA-----GTTCCGCTAAG 309
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Db      1918 GlnGlnLysThrAspLysLysLysPheArgLysGlnGlnLysLeuLysCysAlaSerAsnArg 1937
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Qy      310 AGCAGCTGGCAGATVACGACGAAAGA----- 336
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Qy      337 -----GAAGCAAGTCTTATGACAGGGAAGAAAGATTTCGAA 375
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Qy      376 ATATCTGAGAGAGCATTGTTGAAAGAAACAGAGCTTAACTCAGCTGACAGTTGAG 435
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Db      1976 GlnThrGlnLysLeuMetLysGlnLysLeuGlnValGlnCysGlnAlaGlnLysValArg 1995
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Qy      436 AAGAGCTGAGAGAGGAGCGGAGAGCACTTGAAAAAGAACTTGATCTCAG----- 486
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Qy      517 ---ATGAAAGAGAAATTAAGAAAGAGAGATGAGATGAGATGAAATGTTG----- 567
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Qy      613 GTTACAAAGAGAAATTTACGCTATTAATCAACGTGAGAGAAATTCAGAGCTGGCT 672
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Db      2076 ValProArgPheGlnProLysSerGlnLysGlnThrArgGlnValGln-----GlnLeuAla 2094
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Qy      673 TCTGGGAAATGAGATGTCACAAAGGTGTGTGAGAAATG-----CGCTATCAGCTG 723
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Qy      790 -----AGGATCTGAAATTTAAAGATCAGAGAAATGAGAAATGAGATGAGATGAGAT 843
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Qy      844 -----GAAGCAACCAACACTTGAACAGAGACAGACAGAGAGCCCTGGCC 891
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Qy      892 AGAGAGAGAGCTGAGACTTAACAGAACTGTGGCGGAATCTGAG-----CAC 939
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 Db 2366 GlnLeu 2367  
 RESULT 3  
 US-09-949-016-11433  
 / Sequence 11433, Application US/09949016  
 / Patent No. 6812339  
 / GENERAL INFORMATION:  
 / APPLICANT: VENTER, J. Craig et al.  
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 / FILE REFERENCE: CL001307  
 / CURRENT APPLICATION NUMBER: US/09/949,016  
 / PRIOR FILING DATE: 2000-04-14  
 / PRIOR APPLICATION NUMBER: 60/241,755  
 / PRIOR FILING DATE: 2000-10-20  
 / PRIOR APPLICATION NUMBER: 60/237,768  
 / PRIOR FILING DATE: 2000-10-03  
 / PRIOR APPLICATION NUMBER: 60/231,498  
 / PRIOR FILING DATE: 2000-09-08  
 / NUMBER OF SEQ ID NOS: 207012  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 11433  
 / LENGTH: 2733  
 / TYPE: PRT  
 / ORGANISM: Human  
 / US-09-949-016-11433  
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 Gaps: 24  
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 QY 40 GAAAGCTGAAATTGAGAAATCCCAATTGAAGTTTGAAGAACGACTTACGTAATAT 99  
 Db 1698 GluGluIleArgLeuYsGluAspAenCySerValLeuLyAspGlnLeuArgGlnMec 1717  
 QY 100 CAGAGAACTGTGAAAGTCTTAA-----GAGCACTTAAGCAT----- 138  
 Db 1718 SerIleHleMetGlnGluLeuYsIleAenIleSerArgLeuGlnuHleAspLySglnIle 1737  
 QY 139 -----AAGAAATTTCTTGGCTCTAATACTTGTAAACCGTGTGT 180  
 Db 1738 TrpGlnSerLyAlaGlnThrArgIuValGlnLeuGlnIuYsValCyAspThrLeuGln 1757  
 QY 181 GGTCTTTGTTGAATGTGCTCAGCATGAAGCTGTTCTTTCCCAACCCACTAATGTT 240  
 Db 1758 Gly-----GluAenLySglnLeuLeuSerGlnLeuGlnIuThrArg 1771  
 QY 241 CATATG-----CAGACCATCGAAAGATCGTGTAAAGAAAGATGACTTG 265  
 Db 1772 HleLeuYrHisSerSerGlnAenGlnLeuAlaLeuGlnIuSerGlnLeuYsSerLeu 1791  
 QY 286 ATGTCTGCATGATGTTCCGTAAAGGACAGCTTG----- 318  
 Db 1792 LyAspGlnLeuThrAspLeuSerAenSerLeuGlnYsCySlySglnIuYsGlyAsn 1811  
 QY 319 -----CGAGATACGACGAAAGAGAGAGCAAGTCTTAT 351  
 Db 1812 LeuGlnGlyIleIleArgGlnGlnIuAlaAspIleGlnAenSerLySPhSer---Tyr 1830

QY 352 GAACAGTGAAACMAAGTTTGCATAATCT-----GAGGA 367  
 Db 1831 GluGlnLeuGlnuThrAspLeuGlnIuAlaSerArgGlnLeuThrSerArgLeuHleSglnIu 1850  
 QY 388 GCCAATTTGAAAAACCAAGCTTTA----- 414  
 Db 1851 IleAenMetLySglnIuYsIleIleSerLeuSerGlyLySglnIuAlaIleGln 1870  
 QY 415 ATCCAGTGTGACGATTTGAGAGAGCTGAGAGCGAGCGACTTGAAGAAAGAA 474  
 Db 1871 ValAlaIleAlaGlnLeuYrGlnGlnIuHleAspLySglnIuLeuSglnLeuGlnAenLeu 1890  
 QY 475 CTTGCATCTCAGCAGAGAAAGAGCGCATTTGAGAAAGACATGATGAAAGAAATTAACG 534  
 Db 1891 LeuSerGlnGlnIuGlnIuGlnAenIleValLeuGlnGlnIuYsValAlaAsp 1910  
 QY 535 AAAAGAAAGGATACATGGGATCAAGATTTGATCTTGTCTAGAAATATGGCCCACTG 594  
 Db 1911 LyThrAsnGlnLeuMetGlnuThrLeuYsThrIleLySglnIuAenIleGlnIu--- 1929  
 QY 595 GAGGCCAGGTGAAAGGTTNCAAGAAAGATTTCAAGCTATTAT----- 642  
 Db 1930 LyAlaGlnLeuYsPheValLySerMetSerLeuGlnAenAspArg 1949  
 QY 643 -----CACTGAGAGAA----- 654  
 Db 1950 IleValGlyAspYrGlnGlnIuGlnIuArgHleLeuSerIleIleGlnIuYsAsp 1969  
 QY 655 -----ATTCAAAGCCAGCTGCTTCTCGGAAATGATGTCAAAAGTGTGTGAGAA 708  
 Db 1970 GlnLeuIleGlnIuAlaAlaGlnAenAenLyLeuYsGlnIuIleArgGly--- 1988  
 QY 709 ATCGCTATCAGTGAATAAACCACATGCAAGAGTGAAGGACAGAAAGGACAGACAG 768  
 Db 1989 LeuArgSerHleMetAspLeuAenSerGlnuAlaYsLeuAspAlaGlnLeuIle 2008  
 QY 769 GAGTTGAGCAAAAATTAACAGAGATCTTGAATTAAGAT---CAGGAATATAGAGAA 825  
 Db 2009 GlnIuYrArgGlnAspLeuAenGlnIuIleThrIleLyAspSerGlnIuYsGlnLeu 2028  
 QY 826 TTGAGAAATGAACTGATGAAAGCAAAACA-----CACTTGAACAG 867  
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 Db 2049 LyLeuYsGlnSerGlnIuAlaAenGlnuAspLeuArgYrSerPheAenAlaLeuGln 2068  
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 Db 2069 GlnGlnIuYsGlnAspLeuSerLySglnIleGlnSerLeuYsValSerIleSerGlnLeu 2088  
 QY 952 ACCAGATCTGAAATGACTCACTCACTCAGAA----- 964  
 Db 2089 ThrArg---GlnValIleAlaLeuGlnIuGlnIuYrThrLeuGlnLeuYrHleAlaGln 2107  
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 QY 1060 GGGAGAGTACATGACGATGAAGCAAGGCTTAAGCAGCTGAT----- 1104  
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 QY 1105 ---AAGCAGAGCCAGCCAGCCAGCAGCTGCTG---CAGCTCTTC 1146  
 Db 2168 MetArgAsnIuThrIuThrAlaGlnIuArgValAlaGlnLeuAlaArgAspLeuVal 2187  
 QY 1147 AGCAAGCAGAAACAGCTTCTCTG-----GAGAGCAGAGAGCTGTGGAAGAGTGC 1197

Db 2188 GluMetGluGlnIleuLeuMetValThrIleGluValnIleuSerGluLeuThrAlaGlnIle 2207  
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Db 2208 GlnSerPheGlyArgSerMetSerLeuGlnAsnSer 2220  
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US-09-949-016-6507  
Sequence 6507, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6507  
LENGTH: 3259  
TYPE: PRF  
ORGANISM: Human  
US-09-949-016-6507  
Alignment Scores:  
Pred. No.: 9,44e-15 Length: 3259  
Score: 253.50 Matches: 119  
Percent Similarity: 40.33% Conservative: 104  
Best Local Similarity: 21.52% Mismatches: 179  
Query Match: 9.28% Indels: 151  
Gaps: 24  
US-09-502-945-1 (1-1552) x US-09-949-016-6507 (1-3259)  
Qy 1 CTTCTGGATCATCTCGAAGCTTAAACTTACTTAT-----GAG 39  
Db 2204 ValIleAspGlnIleuLeuSerThrGluArgLysPheSerAlaIleGlnSerIleuGlu 2223  
Qy 40 GAAAGGTGAATTTGAGGAATCCCAATTTGGAATTTTGAAGCAAGCACTTACGTGAATAT 99  
Db 2224 GluGlnIleArgLeuLysGlnAspAsnCysSerValIleuLysAspGlnIleuArgGlnMet 2243  
Qy 100 CAGAGAACTTGTGAAGATCTTAA-----GAGCACTTAAAGCAT-----138  
Db 2244 SerIleHisMetGluGluLeuLysIleAsnIleSerArgLeuGlnIleAspLysGlnIle 2263  
Qy 139 -----AAAGAAATTTCTTGGCTGCTTAACTTGTAACTTGAACCGTTGGT 180  
Db 2264 TrpGluSerLysAlaGlnThrGluValGlnIleuGlnIleuValCysAspThrIleuGln 2283  
Qy 181 GGTCTTGTGTTGAAATGTGCTCAGCATGAGCTGTCTTCCCAACCCACTTAACTTAT 240  
Db 2284 Gly-----GluValnLysGlnIleuLeuSerGlnIleuGlnIleuThrArg 2297  
Qy 241 CATATG-----CAGACCATGAAAGACTGGTTAAAGAAAGAGATGACTTG 285  
Db 2298 HisLeuThrHisSerIleArgIleAsnGlnIleuAlaIleuGlnIleuSerIleu 2317  
Qy 286 ATGTCTGCACTTACTTCCGTAGACAGACTTG-----318  
Db 2318 LysAspGlnIleuThrIleuSerAsnSerIleuGlnLysCysLysGlnIleuLysGln 2337  
Qy 319 -----GCAGATACGACGAAAGAGAGAGAGCAAGCAAGTCTTAT 351  
Db 2338 LeuGlnGlyIleIleIleArgGlnGlnIleuAlaAspIleGlnAsnSerLysPheSer--Tyr 2356

Qy 352 GAACAGTAAACCACTTTTGCATAATATCT-----GAGGA 387  
Db 2357 GluGlnIleuGlnIleuThrAspLeuGlnIleAspArgGluLeuThrSerArgLeuHisGlnIle 2376  
Qy 388 GCCAATTTGAAAAAACAAGCTTAA-----414  
Db 2377 IleAsnMetLysGlnIleuLysIleIleSerLeuSerGlyLysGlnIleuAlaIleGln 2396  
Qy 415 ATCCAGTGTGACAGTTGAGAGAGCTGAGAGCGGACGAGCACTTGAAAAAGAA 474  
Db 2397 ValAlaIleAlaGluLeuArgGlnGlnIleHisAspLysGlnIleLysGlnIleuGlnAsnLeu 2416  
Qy 475 CTTGCATCTCAGCAGAGAAAAAGGCGCATTTGAAAAAGACATGTGAAAAAGAAATAGC 534  
Db 2417 LeuSerGlnIleuGlnIleuGlnIleuValIleuGlnIleuGlnIleuLysValAlaArg 2436  
Qy 535 AAAAGAAAGGAGTACATGGGATCAAAAGATTTGATCTTGTCTCAAAATATGCCCCAATC 594  
Db 2437 LysThrAsnGlnIleuMetGluThrIleuLysThrIleLysGlnIleuAsnIleGlnIle 2455  
Qy 595 GAGGCCAGGTGGAAAAAGTTACAAAGAAAGATTTCAAGCTATTAT-----642  
Db 2456 LysAlaGlnIleuAspSerPheValLysSerMetSerLeuGlnAsnAspArgAspArg 2475  
Qy 643 -----CACTGAGAGAA-----654  
Db 2476 IleValGlyAspArgGlnIleuGlnIleuGlnIleuArgHisLeuSerIleIleuGlnIleuAsp 2495  
Qy 655 -----ATTCAAAGCCAGCTGCTTCCGGAATGATGTCAAAAGCTGTGTGAGAA 708  
Db 2496 GlnIleuIleGlnIleuAlaIleAlaGlnAsnValnLysLeuLysGlnIleuArgGly-- 2514  
Qy 709 ATGCGTATCAGTGTGAATAAACCAATCATGTAGAAAGATGAGCAAGAAAGACACAGA 768  
Db 2515 LeuArgSerHisMetAspAspLeuAsnSerGlnAsnAlaLysLeuAspAlaGluIle 2534  
Qy 769 GAGTTCAGACAAATTAATCAAGGATCTTGAATTTAAAGAT--CAGAAATAGAGAAA 825  
Db 2535 GlnIleuArgGlnAspLeuAsnGlnValIleThrIleLysAspSerGlnIleuLysGlnLeu 2554  
Qy 826 TTGAGAAATGAACTGATGAAAGCAACA-----CACTTGAACAG 867  
Db 2555 LeuGlnIleuAlaGlnIleuGlnIleuAsnLysGlnIleuGlnAsnLysThrAlaLysLeuGlnIle 2574  
Qy 868 GAGCAGCAGAGGACCCCTGGCCAGAGAGATGCTGAGACTAACAGAACTGTGGC 927  
Db 2575 LysLeuLysGlnIleuSerGlnIleuAlaAsnGlnAspLeuArgHisSerPheAsnAlaLeuGln 2594  
Qy 928 GAATCTGAGCACCACCTG-----CACTTC 951  
Db 2595 GluGlnLysGlnAspLeuSerLysGlnIleGluSerLeuLysValSerIleSerGlnLeu 2614  
Qy 952 ACCAGATCTGAATAGCTCACTCAGTCAAGAA-----984  
Db 2615 ThrArg--GlnValThrAlaLeuGlnIleuGlnIleuGlnIleuThrLeuGlnIleuThrHisAlaGln 2633  
Qy 985 -----AAAGATATCATATGATTAATTTGGAAGCTTA-----CAGAG 1023  
Db 2634 LeuLysValnLysGlnIleuGlnIleuAlaHisAspLeuSerAlaLeuPheSerSerGlnLys 2653  
Qy 1024 AGAATGAAATTTGAGAGAACAG-----TGTGTCCACAT-----1059  
Db 2654 ArgIleAlaGlnIleuGlnIleuGlnIleuValCysValGlnLysGlnIleuAlaLysLysVal 2673  
Qy 1060 GGGAGAGTACATGACATGAAGCAAGCAAGGCTTAAAGGCAAGCTGAT-----1104  
Db 2674 GlyGlnIleGlnLysLysLysGlnIleuLysHisIleuHisHisIleAspAlaGlyIle 2693  
Qy 1105 ---AAGCAGACGACGCGCCAGCGGAGCTGCTG--CAGCTCCCTC 1146  
Db 2694 MetArgAsnGlnIleuThrIleuThrAlaGlnIleuArgValAlaGlnIleuAlaAspArgLeuVal 2713

QY 1147 AGCAGCAGACGCTTCTCTG-----GAGAGCAGACCTTCGCGAGAGCTG 1197  
Db 2714 GlnMetGlnLysLeuLeuMetValThrLysGlnLysLeuThrAlaGlnIle 2733  
QY 1198 GACCGGCTCGGAGCCGATTACCGCATGCCACATCT 1236  
Db 2734 GlnSerPheGlnArgSerMetSerLeuGlnAmsSer 2746  
RESULT 5  
US-09-866-108A-15754  
Sequence 15754, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David R.  
APPLICANT: RANK, David K.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OR INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: A60MICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecmca Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 15754  
LENGTH: 1581  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-866-108A-15754  
Alignment Scores:  
Pred. No.: 3,14e-14 Length: 1581  
Score: 246.50 Matches: 104  
Percent Similarity: 41.42% Conservative: 89  
Best Local Similarity: 22.32% Mismatches: 172  
Query Match: 9.02% Indels: 101  
Gaps: 16  
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QY 16 GAGACCTAAACTTACTTATGAGAAAAGTGGAATTGAGAAATCCCAATTGAAGTTT 75  
Db 929 LysArgLeuGlnGlnGlnPheGlnAspLysLeuGlnValGlnGlnGlnAmsGln 948  
QY 76 TTGAGAGACACTTACGTGAATATCAGAGAACTTTCAGATCTTAA-----GAG 126  
Db 949 LeuGlnArgArgLeuGlnAspLeuGlnAlaAspSerLeuGlnArgGlnAlaLeuGln 968  
QY 127 CACTAAGCATAAAGAAATTTCTTCTGCTGCTAATCTTGAACCGTGTGTGT--- 183

Db 969 GlnLeuLysLysLys-----CysGlnArgLeuThrAlaGln 980  
QY 184 -----CTTGTGTTG 192  
Db 981 LeuGlnAspThrLysLeuHisLeuGlnGlnValArgAsnHisGlnLeuGlnLys 1000  
QY 193 AAATGTGCTCAGCATGAGCTGTTCTTCCCAACCATCTAATGTTTCAATATGACAGACC 252  
Db 1001 LysGlnArgArgPheAspSerGlnLeuSerGlnAlaHisGlnLysAlaGlnArgGlnLys 1020  
QY 253 ATC-----GAAAGCTGTTAAAGAAAGATGATGATGCTGCTGCACTGTTCCGTA 306  
Db 1021 LeuGlnArgGlnLysLeuGlnArgGlnLysAspMetLeuLysAlaGlnAlaPheSerLeu 1040  
QY 307 AGGAGCAGCTTG-----GCAGATACGCGAGCAAGAGCAAGT 345  
Db 1041 LysGlnGlnLeuLysGlnLysAspMetAspIleAlaGlyPheThrGlnLysValSer 1060  
QY 346 GCTTATGACAGGTGAACAAAGTT-----TTGCAATATCTGAGAGCCCAATTTTGA 399  
Db 1061 LeuGlnAlaGlnLeuGlnAspIleSerSerGlnLysSerLysAspGlnAlaSerLeuAla 1080  
QY 400 AAACCAAGCTTTAATCCAGTGTGACAGTTGAGAGAGCTGAGAGCGCGAG 459  
Db 1081 LysValLysLys-----GlnLeuArgAspLeuGlnAlaLysValLysAspGlnGln 1098  
QY 460 CGACTTGAAGAAAGACTTGATCT-----CAGCAGAGAAAGGCGCATTTGAG 507  
Db 1099 GlnLeuAspGlnGlnLysLeuThrIleGlnMetLeuGlnGlnAlaLysLeuArgLeuGln 1118  
QY 508 AAAGCATGATGAAAAAGAAATTAACAAAGAGAGTACATGAGATCAAGATGTTG 567  
Db 1119 MetGlnMetGlnArgMetArgGlnThrHisSerLysGln----- 1131  
QY 568 ATCTTCTCAGAAATTTGCCCACTGAGGCCAGCTGAGAAAGGTTACAAAGAAAG 627  
Db 1132 -----MetGlnSerArgAspGlnLysValGlnGlnAlaArg 1143  
QY 628 ATTTGAGCTATTAATCACTGAGAGAAATTCAAAGCCAGCTGCTTCGCGAAATGAG 687  
Db 1144 GlnSerCysGlnLysLysLysLysGlnMetGlnValGlnLeuGlnLysLeuAlaThrLeuSerAsp 1163  
QY 688 GTCAAAAGGTGTGTGAGAAATGCGCTATCAGCTGAATTAACCAACATGAGAGAGAT 747  
Db 1164 LysGlnLysValLysLeuArgGlnLysArgGlnLeuGlnLysLeuAlaThrLeuSerAsp 1183  
QY 748 GAGCAGAAAAGAGCAGACAGAGATTCAAGCAAAAATTAACGAGATCTTGAATTTAA 807  
Db 1184 GlnValAsnArgArgAspPheGlnSerGlnLysArgLeuArgLysAspLeuLysArgThr 1203  
QY 808 GATCAGAAATGAGAAATTAAGATTAAGATCTGATGAAGCAACCAACTTGGAAACAG 867  
Db 1204 LysAlaLeuLeuAlaAspAlaGlnLeuMetLeuAsp-----HisLeu----- 1217  
QY 868 GAGCAGACAGAGCAGCCCTGCGCAGAGAGAGTGCTGATTAACAGAACTGCGGC 927  
Db 1218 -----LysAsnSerAlaProSerLysArgGlnLysAlaGlnLeuLysAsnGlnLeu 1235  
QY 928 GAATCTGAG----- 936  
Db 1236 GlnSerGlnPheThrCysAlaAlaValLysAlaArgLysAlaMetGlnValGlnIle 1255  
QY 937 CACCAATGCACTTCACCGATGTAATTAAGCTCAACTCAGTCAAGAAAAGAGTATCA 996  
Db 1256 GlnAspLeuHisLeu-----GlnIleAspAspIleAlaLysValLysThrAlaLeu 1272  
QY 997 TATGATTAATTTGGAGAAATTAACAGAGAAATTAAGAAATTTGAGAGAACGTGTCCAG 1056  
Db 1273 GlnGlnGlnLeuSerArgLeuGlnArgGlnLysAsnGlnLysIleGln----- 1287  
QY 1057 CATGAGAGATCATGAGACGATGAAGCAAAAGCTTAAGCAGCTGATTAAGCACACCG 1116

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Db      1288 ----AsnArgLeuGluGluAspGlnGluAspMetAsnGluLeuMetLysIleVal 1306
QY      1117 GCCACAGCCAG-----CAGCTGTGTCAGCTCTCTCAGCAAGCAAGCAAGCTT--- 1164
Db      1307 AlaValAlaGlnIleSerArgAspLeuAlaGlnIleAsnAspLeuGlnAlaGlnLeuGlu 1326
QY      1165 -----CTCCGTGAGAGGAGCAGACCTGTCCGAAAGAGGTGAGCCGCTGCCAGCCAGTTA 1218
Db      1327 GluAlaAsnLysGluLysGlnGluLeuGlnGluLysLeuGlnAlaLeuGlnSerGlnVal 1346
QY      1219 CCCAGCATGCTACAAATCT 1236
Db      1347 GluPheLeuGlnGlnSer 1352

RESULT 6
US-09-949-016-10872
/ Sequence 10872, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTNER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10872
/ LENGTH: 1960
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-10872

Alignment Scores:
Pred. No.:      5,91e-14      Length:      1960
Score:          244.00      Matches:      107
Percent Similarity: 40.87%      Conservative: 90
Best Local Similarity: 22.20%      Mismatches: 161
Query Match:      8.93%      Indels:      124
DB:              Gaps:      17

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QY      7 GATGCATCCGAGAGCTAAAGCTTACTTATGAGAAAG----- 45
Db      1409 AspLysLeuGlnIleLysThrArgLeuGlnGlnIleuAspAspLeuValAsp 1428
QY      46 -----TGTGAATTTGAGGAATCCCAATTGAAGTTT----- 75
Db      1429 LeuAspHisGlnArgIleSerAlaCysAsnLeuGlnLysGlnLysPheAspGln 1448
QY      76 -----TTAGGAACGACTTAGATGATATCAGGAAGCTGTGAAAGATCTTAA 123
Db      1449 LeuLeuAlaGlnLysThrIleSerAlaLysIleAlaGlnLysArgAspArgAlaGln 1468
QY      124 GAGCAACTAAGAGATTAAGAAATTTCTTGTGCTGATTAATCTTGAACCGTGTGGTGT 183
Db      1469 AlaGlnAlaArgLysGlu-----ThryAla 1478
QY      184 CTTTGTGTAATGTGCTCAGATGAAGCTGTTCTTCCCAACCCATTAATGTTGAT 243
Db      1479 LeuSerLeuAlaArgAlaLeuGlnLysAlaMetGlnGlnLysAlaGln----- 1494
QY      244 ATGCAGACCATCGAAAGATCGGTAA-----GAAAGATGATCTGATGCT 291
Db      1495 -----LeuGlnIleGlnLeuAsnLysGlnPheArgThrGlnMetGlnAspLeuMetSer 1511

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QY      292 GCACATAGTTTCCGTAAAGAGCACTTGCGCATACGACCAAGCAAGCAAGCTTAT 351
Db      1512 SerLysAspAspValGlnLysSerValHisGlnLeuGlnLysSerLysArgAlaLeuGln 1531
QY      352 GAACAGGTGAACCAAGT-----TTGCAAAATATCT 381
Db      1532 GlnGlnValGlnGlnMetLysThrGlnLeuGlnLysGlnLysAspGlnLeuGlnAlaThr 1551
QY      382 GAGGAAGCC-----AATTTGAAAAAACCAGGCTTTAATC----- 417
Db      1552 GluAspAlaLysLeuArgLeuGlnValaLeuLeuGlnAlaMetLysAlaGlnPheGluArg 1571
QY      418 -----CAGTGTACCACTTGAGAGAGAGCTGAGAGGCGG 456
Db      1572 AspLeuGlnGlnLysArgAspGlnGlnSerGlnGlnLysLysGlnLeuValArgGlnVal 1591
QY      457 GAGCGACTTGAAAAAGCACTTGATTCAGCAAGAAAGAGGCGCATTGAGAAAGCATG 516
Db      1592 ArgGlnMetGlnAlaGlnLeuGlnLysArgLysGlnArgSerMetAlaValAlaAla 1611
QY      517 ATGAAAAAGAAATAACGAAAGAGGAGTACATGGATCAAAAGATGTTGATCTTGTCT 576
Db      1612 ArgLysLys-----LeuGln 1616
QY      577 CAGAAATATTTGCCCACTGAGAGGCCAGGTGAAAGGCTTACAAAGAAAGATTTCAGCT 636
Db      1617 MetAspLeuLysAspLeuGlnAlaHisValAspSerAlaAsnLysAsnArgAspGlnAla 1636
QY      637 ATTAATCACTGAGGAATTTCAAAAGCCAGT-----GCTTCGGGAAATGATGTC 690
Db      1637 IleLysGlnLeuArgLysGlnGlnAlaGlnMetLysAspCysMetArgGlnLeuAspAsp 1656
QY      691 ACAAGGTGTGTGAGAAATGCGCTTATCAGCTGAATTAACCAAC----- 735
Db      1657 ThrArgAlaSerArgGlnGlnIleLeuAlaGlnAlaLysGlnAsnLysLysLeuLys 1676
QY      736 -----ATGAGAAAGATGAGCGCAAGAAAGCAAGACAGACAG 771
Db      1677 SerMetGlnAlaGlnMetIleGlnLeuGlnGlnIleuAlaAlaAlaGlnArgAlaLys 1696
QY      772 TTCAGAGCAAAAACTAAACGAGATCTTGAATTAAGAT----- 810
Db      1697 ArgGlnAlaGlnGlnLysArgAsp-----GlnLeuAlaAspGlnIleAlaAsnSerSerGly 1715
QY      811 -----CAGGAATATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 852
Db      1716 LysGlnAlaLeuAlaLeuGlnLysLysArgArgLeuGlnAlaArgIleAlaGlnLeuGln 1735
QY      853 CAACACTTGGAACAGAGAGAGCAAGAGAGCCCTGCGCAAGAGAGAGTGCCTGAGACTA 912
Db      1736 GluGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1755
QY      913 ACAGAACTGTGGGCGAATCTGAGCAACCACTGCACCTGCACGATCTGAATATGCTCA 972
Db      1756 AsnLeuGlnIleAspGlnIleAsnThrAspLeuAsnLeuGlnLysSerHis--AlaGln 1774
QY      973 CTCAGTCAAGAAAAAGGTATACATATGATTAATTGGAAAGTTACAGAGAAATGAA 1032
Db      1775 LysAsnGlnAsnAlaArgGln-----GlnLeuGlnArgGlnAsnLys 1788
QY      1033 GAATTGAGAGAACAGTGTCTCAGATGGAGAGTACATGAGACGATGAAGCAAGAGCTA 1092
Db      1789 GluLeuLys-----ValLysLeuGlnGlnMetGlnGlnThrValLysSerLysTyr 1805
QY      1093 AGCAGACTGATTAAGACAGAGCCAGCCAGACCAAGCACTGTGTGACGCTCCACAG 1152
Db      1806 LysAlaSerIleThrAlaLeuGlnLysIleAlaGlnLeuGlnLysLeuAspAsn 1825
QY      1153 CAGAACAGCTTCTCTGAGAGGAGAGCTGTCCGAAGAGGTGAGCCGTCGCGAGC 1212
Db      1826 GluThrLys-----GlnArgGlnAlaAlaCysLysGlnValaLysArgThrGlnLys 1842
QY      1213 CAGTTA 1218

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Db      1843 Lvleu 1844
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RESULT 7
US-09-538-092-1077
/ Sequence 1077, Application US/09538092
/ Patent No. 6753314
/ GENERAL INFORMATION:
/ APPLICANT: Glot, Loic
/ TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
/ FILE REFERENCE: 15966-542
/ CURRENT APPLICATION NUMBER: US/09/538,092
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/127,352
/ PRIOR FILING DATE: 1999-04-01
/ PRIOR APPLICATION NUMBER: 60/178,965
/ NUMBER OF SEQ ID NOS: 1387
/ SOFTWARE: CuraPatSeqFormatter Version 0.9
/ SEQ ID NO 1077
/ LENGTH: 1960
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (0)..(0)
/ OTHER INFORMATION: Polypeptide Accession Number P35579
US-09-538-092-1077

Alignment Scores:
Pred. No.: 7,33e-14      Length: 1960
Score: 243.00           Matches: 106
Percent Similarity: 40.87%      Conservative: 91
Best Local Similarity: 21.99%    Mismatches: 161
Query Match: 8.89%             Indels: 124
DB: 4                     Gaps: 17

US-09-502-945-1 (1-1552) x US-09-538-092-1077 (1-1960)
QY      7 GATGATCCGAGAACTTAATTAAGGAAAG-----45
Db      1409 AsplyleuGlulubylserThrArgLeuGlnGluLeuAspLeuValAsp 1428
QY      46 -----TTGAAATTGAGAAATCCCAATGAAGTT-----75
Db      1429 LeuAspHisGlnArgInserAlaCysAsnLeuGluLysGlnPheAspGln 1448
QY      76 -----TTGAGAAAGCACTTAGTGAATATCAGAGAACTTGTAAGATCTTAA 123
Db      1449 LeuLeuAlaGluLysThrIleSerAlaLysTyrAlaGluGluArgAspAlaGlu 1468
QY      124 GAGCACTTAAGCATTAAGATTCTTGGCTGCTAATCTTGAACCGTGGTGGT 183
Db      1469 AlaGluAlaArgGluLysGlu-----ThryAla 1478
QY      184 CTTTGTGAAATGTGTCAGCATGAAGCTGTTCTCCCAACCCATTAATGTTGAT 243
Db      1479 LeuSerLeuAlaArgAlaLeuGluGluAlaMetGluGlnLysAlaGlu-----1494
QY      244 ATGACAGACCTGAAAGAGCTGTTAA-----GAAAGAGTACTGATGTC 291
Db      1495 -----LeuGluArgLeuAsnLysGlnPheArgThrGluMetGluAspLeuMetSer 1511
QY      292 GCACTAGTTCCCTTAAGACAGCTTGAGCATACGAGATAACGAAAGAAAGCAAGTCTTAT 351
Db      1512 SerLysAspArgValGluLysSerValHisGluLeuGluLysSerLysArgAlaLeuGlu 1531
QY      352 GAACAGCTGAACAAGT-----TGCAAAATATCT 381
Db      1532 GlnGlnValGlnGluMetLysThrGlnLeuGlnGluLeuGluAspGluGlnAlaThr 1551
QY      382 GAGGAAGCC-----AATTTGAAAAAACCAAGGCTTAATC-----417

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Db      1552 GluAspAlaLysLeuArgLeuGluValAsnLeuGlnAlaMetLysAlaGlnPheGluArg 1571
QY      418 -----CAGTGTGACCACTTAGAGAGAGCTGAGAGCGCGC 456
Db      1572 AsplLeuGlnGlyArgAspGluGlnSerGlnLysLysGlnLeuValArgGlnVal 1591
QY      457 GAGCAGCTTGAAGAAAGCACTTGATCTCAGCAAGAGAAAGGCGCATTTGAGAAAGCATG 516
Db      1592 ArgGluMetGluAlaGluLeuGluAspGluArgLysGlnArgSerMetAlaValAla 1611
QY      517 ATGAAAAAGAAATTAAGAAAGAGAGACTACATGGATCAAGATGTTGATCTGCT 576
Db      1612 ArgLysLys-----LeuGlu 1616
QY      577 CAGAAATTTGCCCACTGAGGCCCAAGTGGAAAGATTACAAAGAAAGATTTCAGCT 636
Db      1617 MetAspLeuLysAspLeuGluAlaHisIleAspSerAlaAsnLysAsnArgAspGluAla 1636
QY      637 ATTAATCACTGGAGAAATTCAAGCCAGCTG-----GCTTCTGGGAAATGATGTC 690
Db      1637 IleLysGlnLeuArgLysLeuGlnAlaGlnMetLysAspCysMetArgGluLeuAspAsp 1656
QY      691 ACAAGGTGTGTGAGAAATGCGCTATCAGCTGAATTAACCAAC-----735
Db      1657 ThrArgAlaSerArgGluGluIleLeuAlaGlnAlaLysGlnLysLysLeuLys 1676
QY      736 -----ATGAGAGAGATGAGCCAGAAAGAGCAGACAGAG 771
Db      1677 SerMetGluAlaGluMetIleGlnLeuGlnGlnLysAlaAlaAlaGluArgAlaLys 1696
QY      772 TTCAGAGCAAAATTAACAGGATCTTGAATTAAGAT-----810
Db      1697 ArgGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1715
QY      811 -----CAGAAATAGAGAAATTGAGAACTGATGAAGCAAA 852
Db      1716 LysGluAlaLeuAlaLeuGlnGluLysArgArgLeuGlnLysAlaAlaGlnLeuGlu 1735
QY      853 CAACACTTGAGACAGAGCAGCAAGAGCCCTGCGCCAGAGAGAGTCCAGACTA 912
Db      1736 AsnLeuGlnIleAspGlnIleAsnThrAspLeuAsnLeuLysSerHis--AlaGln 1755
QY      913 ACAGAACTGTGGCGCAATCTGAGCAACAATGACCTGACAGTCTGAATATGACTCA 972
Db      973 CTCAGTCAAGAAAAAGTATACATATGATTAATTGGAAAGTTACAGAGAAATGAA 1032
Db      1775 LysAsnGlnAsnAlaArgGln-----GlnLeuGluArgGlnAsnLys 1788
QY      1033 GAATTGAGAGACAGTGTGTCAGCATGGAGAGTACATGAGCGATGAAGCAAGCTA 1092
Db      1789 GluLeuLys-----ValLysLeuGlnGlnLysGlnGluLysSerLysTyr 1805
QY      1093 AGGACAGCTGATAGACAGCCAGCCAGAGCTGAGCTGTCAGCAG 1152
Db      1806 LysAlaSerIleThrAlaLeuGluAlaLysIleAlaGlnLeuGluGlnLeuAspAsn 1825
QY      1153 CAGAACAGCTTCTCTGAGAGAGCAGAGCTGTGCAAGAGGTGACCGCTGCGGACC 1212
Db      1826 GluThrLys-----GluArgGlnAlaAlaCysLysGlnValArgArgThrGlnLys 1842
QY      1213 CAGCTTA 1218
Db      1843 Lvleu 1844

RESULT 8
US-09-538-092-1252
/ Sequence 1252, Application US/09538092
/ Patent No. 6753314
/ GENERAL INFORMATION:
/ APPLICANT: Glot, Loic

```





```

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPacSeqFormatter Version 0.9
; SEQ ID NO 1078
; LENGTH: 1976
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P35580
US-09-538-092-1078

Alignment Scores:
Pred. No.: 1,26e-13 Length: 1976
Score: 240.50 Matches: 115
Percent Similarity: 46.01% Conservative: 104
Best Local Similarity: 24.16% Mismatches: 148
Query Match: 8.80% Indels: 109
DB: Gaps: 23

US-09-502-945-1 (1-1552) x US-09-538-092-1078 (1-1976)

QY 7 GATGCATCCGAGAGCTAAATCTTATGAGAAAAGTGTGAATTAAGAAATCCCAA 66
DB 1038 Asplenglunlglnuglueylslyglulglulthrarglninglueglulysalys 1057
QY 67 TTGAAGTT-----TTGAGAACACTTACTGTAATTCAGAGAACT 108
DB 1058 ArglyseuabepelgluthrthrAspleuglnbeplnlealaglueglulagl 1077
QY 109 TGTGAAGATCTTAAAGCACTAAAGCATTAAGATTTCTTCTGCGTCT----- 159
DB 1078 llaepglueuylseuglnleualalyelsglulglueuglnglyalaleuala 1097
QY 160 -----AATCTTAAACCGTGTGTGTCTTTGTGAATGTCTCAGCAT 207
DB 1098 ArgglyAsrAspRluthrleuHlelyeAsnAbnAlaleuylsVal---ValArgglueu 1116
QY 208 GAAGCTGTTCTTCCCAACCCATATGTTTCATATGCAGACCATCGAAAG----- 261
DB 1117 GlnAlaglInllealaglueuglnglnAspPheglueRglulysalaserArgAsnlye 1136
QY 262 CTGTTAAAGAAAGATGATGATGTCTGCACCTAGTTCCGPAAGAGCAGCTGGCA 321
DB 1137 AlagluylseglulnyAsrAspleuSerGlugluueglulAlaleuylsrngluueglu 1156
QY 322 GATACCGACGAAAGAGAGCAAGTCTTATGAA---CAGGTGAACAAGTTTGCATAA 378
DB 1157 AspThrleuAspThrThrAlaAlaglInglInleuAsrThrlyAsrAsgluglnVal 1176
QY 379 TCTGAG-----GAGCCAAATTTGAAAAACCAAG-----GCTTAAATCCAG--- 420
DB 1177 AlagluylseuylsAlaleuglnglulgluthrlyAsnHlsglulaglInlleAsp 1196
QY 421 -----TGTACCAAGTTGAGAGAGAGCGTGCAGAGCAGCG 456
DB 1197 MetArgglInArgHlvalatThrAlaleuGlugluueSerGlugluInleuGlIn---GlnAla 1215
QY 457 GAGCGACTTGAAGAAAGCTTGATCTCAGCAAGAGAAAGGGCCATTGAGAAAGCAG 516
DB 1216 LysArgPheylsAlaleuLeu-----GluylsAbnlysglnglyleuglngluthrAsp--- 1232
QY 517 ATGAAAAAGAAATTAACGAAAGAAAGGAGTACATGGATCAAGATTTGATCTTCT 576
DB 1233 ---AsnlysglueuAlaCyRglu-----VallysvAlleugln 1244
QY 577 CAGATATTCGCCCACTGAGAGCCAGGTGAAAGGTTACAAAGAAAGATTCAGCT 636
DB 1245 GlnVallyAlalegluSerGlulHllyb---ArglyblybAleAspAla 1259
QY 637 ATTAATCACTGAGGAATTAACAAGCCAGCTGCTTCGGGAA-----ATGAT 687
DB 1260 -----GlnValnglnglueuHleAlalyValserGlugluysAsrArgleuArgValglu 1277
```

```

QY 688 GTCCAAAGGTGTGTGGAAGAAATGCGCTATCAGCTGATATAAAACAATGAGAAAGAT 747
DB 1278 LeuAlagluylsAlaserlyleuglnAsnglInleuAspAsnAlaserThrleuGluln 1297
QY 748 GAGCGAGAAAGAGCAAGAGATTCAGAGCAAAAATTAACAGGATCTTGAATTA 807
DB 1298 Glulagluylslysglylelysphe---AlalyAspAlalaserleuglnglueglIn 1316
QY 808 GATCAGAAATTAAGAAATG----- 828
DB 1317 leuGlnAspThrnglnglueuglnglulthrArglnglnlyseuAsnleuSerSer 1336
QY 829 AGATA---GAATCGATGAAGCAAAACAACACTTGAACAGAGCAGAGAGCAGCC 885
DB 1337 ArgllleRgslInleuglnglulysAsnSerleuInglInglIngluglu 1356
QY 886 CTGCGCCAGA----- 894
DB 1357 GlulAlarglybAsnleuglnglnValleuAlaleuInserglInleuAlAspThr 1376
QY 895 -----GAGAGTCCCTGAGACTTAACAGAACTCTGGCCGAATCTGAGACCAA 942
DB 1377 LyslyblybValAspAspleuGllyThrllleglserleuInglulAlalyblyb 1396
QY 943 CTGCACTCACAGATCTGAATAGCTCACTCAGTCAAGAAAAGGTATATATAT 1002
DB 1397 LeuileuylsAspAlagluAlaleuSerGlnArgleuInglulysAlaleuAlalybAsp 1416
QY 1003 AAATGGAAAGTTACAGAGAGA---AATGAAGATTTGAGAGAAAGTGTCTCAGCAT 1059
DB 1417 LysleuglnglulysThrlybAsnArgleuglnglnleuAspPheleuThrVal----- 1434
QY 1060 GGGAGACTACATAGACAGATGAAGCAAGGCTTAAGCAGCTGTGATAGCACACCGAGCC 1119
DB 1435 -----AspleuAsp---HisGlnArgGln 1441
QY 1120 ACAGCCAGCAGCTGGTGCAGCTCTCAGACAGACAGACAGCTTCTCGAGAGAGCAG 1179
DB 1442 ValAlaserAsnleuglnglulysGlnlyblybPheAspGlnleuAlagluyls 1461
QY 1180 AGCCTGTG-----GAAGAGTGAACCGCTGCGGACCCAG 1215
DB 1462 SerllleSerAlarglyrAlagluArgAspArgAlagluAlaglu 1477

RESULT 10
US-09-595-684B-31
; Sequence 31, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Onashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2662
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-31

Alignment Scores:
Pred. No.: 1.77e-13 Length: 2662
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Db      1057 AspglnAsnAsnArgLeuLysGlnLysValAsnGlnAspSerLeuLysGln 1076
Qy      97  TATCAAGAACTTGTGAAGATCTTAAAGACAACTAAAGCATTAAGATTTCTTGAGCT 156
Db      1077 LysGlnThrLeuLeuLeuGlnGlnLysGlnGlnLeuGlnLysAsnValThrLeuAsp 1096
Qy      157  GCTAATATCTTGAAACCGGTGTGGTGT-----CTTTGTTGAAATGT 198
Db      1097 ValGlnIleGlnHisValIleGlnLysArgAlaLeuSerGlnLeuThrGlnLysVal 1116
Qy      199  GCTCAGCATGAACTGTCTTCTCCCAACCATATGATATGATATGACACCATGCA 258
Db      1117 ThrCysTyrLysAlaLysIleLysGlnLeuGlnThrIleLeuGlnThrGlnLysValGln 1136
Qy      259  AGA-----CTGCCTTAAGAAAGAGATGACTGATG-----TCGCATGATGTTCC 303
Db      1137 ArgSerHisSerLysLysLeuGlnLysGlnAspIleLeuGlnLysGlnSerIleIleLeuLys 1156
Qy      304  GTAAGAGCAGCTTGGCAGATACGCAAGAAAGAAAGAGAGCTTATGAAACAGGTGAAA 363
Db      1157 LeuGlnLysArgAsnLeuLysGlnPheGlnGlnHisLeuGlnLysAspSerValLysAsnThrLys 1176
Qy      364  CAAGTT-----TTGCAATATCTGAGAAAGCC-----AATTTT 396
Db      1177 AspLeuAsnValLysGlnLeuLysLeuLysGlnGlnIleThrGlnLeuThrAsnAsnLeu 1196
Qy      397  GAAAAAACCAAGCACTTATTCAGATGACAGTGTGAGAGAGCTGAGAGCTGAGACAG--- 453
Db      1197 GlnAspMetLysHisLeuLeuGlnLysGlnGlnLysGlnGlnLysGlnLysGlnLysGln 1216
Qy      454  GCGGAGCGACTTGAAGAAAGACTT--GCATCTCAGCAGAGAAAGAGCGCATTTGAGAAA 510
Db      1217 ThrGlnLysLeuLysGlnGlnLysSerAlaSerSerAlaArgThrGlnAsnLeuLysAla 1236
Qy      511  GACATGATGAAAAAGGAAATACGAAAGAAAGAGAGTGCATGAGTGAAGATGTTGATC 570
Db      1237 AspLeuGlnArg-----LysGlnGlnAspTyrAlaAsp----- 1247
Qy      571  TTGTCTCAGAAATATTCGCCCACTGAGAGCGCCAGGTGAGAAAGCTTAAAGAAAGATT 630
Db      1248 LeuLysGlnLysLeuThrAspAlaLysLysGlnIleLysGlnValGlnLysGln---Val 1266
Qy      631  TCAGCT-----ATTAATCAACTGAGAGAAATT 657
Db      1267 SerValMetArgAspGlnAspLysLeuLeuArgIleLysIleAsnGlnLeuGlnLysLys 1286
Qy      658  CAAAGCAGCTGCTCTCGGAAATGATGTC---ACAAAGGTGTGTGAGAAATGCCG 714
Db      1287 LysAsnGln---CysSerGlnGlnLeuAspMetLysGlnArgThrIleGlnGlnLysLys 1305
Qy      715  TATCAGCTGATATAACCAATGAGAGAGATGAGAGAGAAAGAGAGACACAGAGATTG 774
Db      1306 GlnGlnLeuAsn-----AsnGlnLysValGlnGlnAlaIleGlnGlnTyrGln----- 1321
Qy      775  AGAGCAAAAACTAACAGGATCTTGAATTAAGATCAAGAAATGAGAAATTTGAGAAATA 834
Db      1322 -----ArgLacCysLysAspLeuAsnValLysGlnLysIleIleGlnAspMetArgMet 1339
Qy      835  GAATCGATTAAGAAAGCAAAACACTTGGAACAGAGAGACAGAAAGGACCCCTGGCCAGA 894
Db      1340 ThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1359
Qy      895  GAGAGAGCTGAGACTA---ACAGAACTGCTGGGCGAATCTGAGCACAACATGACCTC 951
Db      1360 GlnGlnValGlnLysGlnLysAlaThrGlnLeuGlnLysLysTyrLysGlnLysCysAsnAspLeu 1379
Qy      952  ACCAGATCTGAAATATCTCAACTCAGTCAAGAAAGAAAGAGTATCATATGATTAATTGGGA 1011
Db      1380 GlnThrLysAsnAsnGlnArgSerAsnLysGlnHisLeuGlnAsnThrAspValLeuGln 1399
Qy      1012 AAGTTACAGAGAAATGAGAA----- 1035

```

```

Db      1400 LysLeuThrAsnLeuGlnAspGlnLeuGlnGlnSerGlnGlnLysTyrAsnAlaAspArg 1419
Qy      1036 -----TTGAGAGAACAGTGTGTCCAGCATGGGAGAGTACATGACGATGAAGCAA 1086
Db      1420 LysLysTyrLeuGlnGlnLysMetMetLeuIleThrGlnAlaLysGlnLysGlnLys 1439
Qy      1087  AGGCTTAAGCAGCTGGATTAAGCAGAC-----CAGGCCACA 1122
Db      1440 ArgAsnLysGlnMetLysTyrAlaGlnAspArgGlnLysPhePheLysGlnGlnAsn 1459
Qy      1123  GCCCAGCAGTGGTGT-----CAGCTCTCAGAGACAGAACAGAGCTTCTCGTGAAGAG 1176
Db      1460 GlnMetGlnIleLeuThrAlaGlnLeuThrGlnLysAspSerAspLeuGlnLysTyrArg 1479
Qy      1177  CAGAGCCTGTGGAGAGAGTGAACCGGCTGGGAGCCAGTACCCAGTACCCACAATCT 1236
Db      1480 GlnGlnLysArgAspGlnLeuValAlaAlaLeuGlnIleGlnLeuLysAlaLeuLysSer 1499
Qy      1237  GAT 1239
Db      1500  Asn 1500

```

## RESULT 13

```

US-09-949-016-7880
/ Sequence 7880, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTNER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7880
/ LENGTH: 1786
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-7880

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## Alignment Scores:

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Pred. No.: 1,86e-13 Length: 1786
Score: 238.50 Matches: 108
Percent Similarity: 44.47% Conservative: 97
Best Local Similarity: 23.43% Mismatches: 179
Query Match: 8.73% Indels: 77
DB: 4 Gaps: 19

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US-09-502-945-1 (1-1552) x US-09-949-016-7880 (1-1786)

```

Qy      37  GAGCAAAAGTGTGAATTAAGATCCCAATGAAATTTTGAAGAAAGCACTTACGTGAA 96
Db      1063  AspglnAsnAsnArgLeuLysGlnLysLysLysLysLysLysLysLysLysLysLys 1082
Qy      97  TATCAGAAAGCTTGTGAAGATCTTAAAGACAACTAAAGCATTAAGAAATTTCTTGAGCT 156
Db      1083  LysGlnThrLeuLeuLeuGlnGlnLysGlnGlnLysGlnGlnLysAsnValThrLeuAsp 1102
Qy      157  GCTAATATCTTGAAACCGTGTGGTGT-----CTTTGTTGAAATGT 198
Db      1103  ValGlnIleGlnHisValIleGlnLysArgAlaLeuSerGlnLeuThrGlnLysVal 1122
Qy      199  GCTCAGCATGAAAGCTTCTTCTCCAAACCATATGATATGATATGACACCATGCA 258
Db      1123  ThrCysTyrLysAlaLysIleLysGlnLeuGlnThrIleLeuGlnThrGlnLysValGln 1142

```

QY	259	AGA-----CTGTTTAAAGAAAGATGACCTTGAAG-----TCGACACTAGTTCC	303
Db	1143	ATGserHisSerrAlaLysLeuGluGlnAspIleLeuGluLysGluSerIleIleLeuLys	1162
QY	304	GTAAGAGACACCTTGGCAGATACCGACGAAAGAGACAGACAGCTTATGAACAGGTGAA	363
Db	1163	LeuGluATGAsnLeuLeuGluPheGluGlnIuHileuGlnAspSerValLysAsnThrLys	1182
QY	364	CAAGTT-----TTCGCAATATCTGAGAGCC-----AATTTT	396
Db	1183	AspLeuAsnValLysGluLeuLysLeuLysGluGlnIleThrGlnLeuThrAsnAsnLeu	1202
QY	397	GAAGAAACCAACGCTTAAATCCAGTGTACCAAGTTGAGAAAGAGCTGGAAGCAGC---	453
Db	1203	GlnAspMetLysHisLysLeuGlnLeuLeuLysGluGlnGluGlnGluThrAsnArgGlnLys	1222
QY	454	GCGGAGCAGCTTGAAGAAAGAACTT---GCATCTCGACAAAGAGAAAGGCGCATTGAGAA	510
Db	1223	ThrGluLysLeuLysGluGlnLeuSerLysAsnSerrAlaArgThrGlnAsnLeuLysAla	1242
QY	511	GACATGATGAAAGAAAGAAATTAAGAAAGAGAGTACATGGATCAAGAGATGTGATC	570
Db	1243	AspLeuGlnArg-----LysGluGlnAspTyrAlaAsp-----	1253
QY	571	TTTGCTCAGAAATATTGCCCACTGGAGGCCCGAGGTGGAGAAAGGTTACAAAGAAAGATT	630
Db	1254	LeuLysGlnLysLeuThrAspAlaLysLysGlnIleLysGlnValGlnLysGlu---Val	1272
QY	631	TCAGCT-----ATTAAATCAACTGAGAGAAATT	657
Db	1273	SerValMetArgAspGluAspLysLeuLeuArgIleLysIleAsnGluLeuGluLysLys	1292
QY	658	CAAGCCAGCTGGCTTCTCGGAAATGAGATGC--ACAAAGGTGTGTGAGAAATGGCG	714
Db	1293	LysAsnGln---CysSerGlnGlnLeuAspMetLysGlnArgThrIleGlnGlnLeuLys	1311
QY	715	TATCAGCTGATTAACCAACATGAGAAAGATGAGCGAGAAAGAGACACAGAGATTC	774
Db	1312	GluGlnLeuAsn-----AsnGlnLysValGlnGluAlaIleGlnGlnTyrGlu-----	1327
QY	775	AGAGCAAAATCTAACAGGATCTTGAATTAAGTACGAAATAGAGAAATTTGAGATA	834
Db	1328	-----ArgAlaCysLysAspLeuAsnValLysGluLysIleIleGluAspMetArgPheC	1345
QY	835	GAACCTGATGAAAGCAACCAACACTTGGACAGGACGACGAAAGGACCCCTGGCCGA	894
Db	1346	ThrLeuGluGlnGlnGlnGlnIleThrGlnValGluGlnAspGlnValLeuGluAlaLysLeu	1365
QY	895	GAGAGTGCCTCGAGACTA--ACAGAACTGCTGGCGCAATTTAGACCAACTGCACCTC	951
Db	1366	GluGlnValGluArgLeuAlaThrGluLeuGlnLysTyrLysGlnLysCysAsnAspLeu	1385
QY	952	ACCAAGATCTGAAATAGCTCAACTCAGTCAAGAAAGAAAGCTTACATATGATTAATTTGGG	1011
Db	1386	GluThrLysAsnAsnGlnArgSerrAsnLysGlnHisLysGluAsnAsnThrAspValLeuGly	1405
QY	1012	AAGTTACAGAGAAAGAAATGAAGAA-----	1035
Db	1406	LysLeuThrAsnLeuGlnAspGluLeuGlnLeuSerGluGlnLysTyrAsnAlaAspArg	1425
QY	1036	-----TTGAGAGAACTGTGTCCAGCATGGGAGAGTACATGAGACATAGAACAA	1086
Db	1426	LysLysTyrLysLeuGlnGlnLysMetMetLeuIleThrGlnAlaLysGluAlaGluAsnIle	1445
QY	1087	AGCGTAAGGCACTCGATTAACACAGC-----CAGGCCACA	1122
Db	1446	ArgAsnLysGluMetLysLysTyrAlaGluAspArgLysArgPheLysGlnGlnAsn	1465
QY	1123	GCCGACGACGCTGTG-----CAGCTCTCAGACAGACGAACGACTTCTCTGAGAGG	1176
Db	1466	GluMetGluIleLeuThrAlaGlnLeuThrGluLysAspSerrAspLeuGlnLysTyrArg	1485
QY	1177	CAGAGCTGTGCGAAGAGGTGGAACCGGCTGGCAGACCACTTAACCCAGCATGCCCAATCT	1236

[illegible]

```

OY      424  GACCAAGTTAGAGAAAGCTGGAGAGGCGAGCGACACTTGAAGAAAAGAACTTGACACTT 483
Db      677  GtmetwetiPheGlnArgleuGlnlysetulargtGluSerGluGluSerIleuThr 696
OY      484  CAGCAAGACAAAAGGCCATTGAGAAAGACATGATGAAAAGAAATTAAGAAAGAAAG 543
Db      697  SerIySeValThrLeuIyGluGlnGlnIhIseGlnleuGluIyGluLeuThrAspGlnIly 716
OY      544  GAGTACATGACGA-----TCAAGATGTTGATCTTGCTCAGAAATATATGCCCAACTG 594
Db      717  SerIySeValwaspGlnValleuSerIySeValleuValaAlaGluGluArgValArgThrIleu 736
OY      595  GAGGCCCAAG-----GTGGAAAAGTTTCAAGAAAAGAAAGATTTCAGCTATTATATCA 645
Db      737  GlnGluGluGluArgTyrTrpCysGluSerIleuGluIySerThrLeuSerGlnThrIyAspGln 756
OY      646  CTGAGAGAAATTCAAAGCCAGCTGGCTTCTCGGGA-----ATGATGTCAAAAG 696
Db      757  LeuSerGlnIyArgGluGlnGlnIleuValGluIySerGlyGluLeuLeuValaleuGlnIly 776
OY      697  GTGTGTGAGAAATGCGGTATCAGTGA-----AATTAACAACATGAGAGAG 744
Db      777  GluAlaAspSerMetCysArgAlaAspPheSerIleuLeuArgAspGlnPheLeuThrIyArg 796
OY      745  GATGAGCGAAGAAAAGACACAGAGATTCAGAGCAAAAAGCTTAACAGGATCTTGAATT 804
Db      797  LysIySeValIaGluIyGln-----ValAlaSerIleuIyGluAlaleuIySeIle 812
OY      805  AAAGATCAAGAAATAGAGAAATTTGAGAAATAGAACTGGATGAAGCAAAACAACACTTGGAA 864
Db      813  GlnArgSerGlnLeuGlu-----LysAsnLeuLeuGlu 823
OY      865  CAGGAGCGACGACGAAGCGCCCTGCGACAGAGAGAGTGCCTGAGACTTAACGAATGCTG 924
Db      824  GlnIySeGlnGluAsnSerCysIleGlnIySeGlu-----MetAlaThrIleuLeuVal 841
OY      925  GGCGAATCTGAGCACCAACTGCACTTCACAGATCTGAATTAAGTCAACTCAGTCAAGAA 984
Db      842  AlaGlnAspAsnIhIseGlu-----ArgAlaArgIyLeuMetIyGluLeuAsnGln--- 858
OY      985  AAAAGCTTATCAATATGATAAATTTGGAAAAGTTTACAGAGAGAAATGAAGAATTTGAGAAA 1044
Db      859  MetGlnTyrGlnIyTyrThrGluLeuIySeIyGlnMetAlaAsnGlnIyAspLeuGluIyArg 878
OY      1045  CAGTGTGTCCAGCATGGGAGAGTACATGACAGAGAAAGCAAAAGGCTTAAGCAGCTGGAT 1104
Db      879  ArgGlnMetGluIleSerAspAlaMetCysThrIleuIySeSerGluValIyAspGluIle 898
OY      1105  AAGCAGACCCAGAGTCACAGCCACGACGCTGTGACGCTCTTCAGCAAGACAGAACGCTT 1164
Db      899  ArgThrSerIleuIyAsnLeuAsnGlnPheLeuProGluLeuProAlaAspLeuGluAla 918
OY      1165  CTCCTGGAGAGG---CAGAGCTGTGTGGAAAAGGTGAGACCGGCTCGGACCCAGTTACCC 1222
Db      919  IleuGlnIyArgAsnGluAsnLeuGlnIyGluIleuGlnSerIleuIySeIyAsnLeuPro 938

RESULT 15
US-09-538-092-918
; Sequence 918, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Manafield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387

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: SOFTWARE: CuraPacSeqFormatter Version 0.9
: SEQ ID NO 918
: LENGTH: 1937
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)..(0)
: / OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918

Alignment Scores:
Pred. No.:      2.66e-13      Length:      1937
Score:          237.00       Matches:      112
Percent Similarity: 41.07%   Conservative: 88
Best Local Similarity: 23.00% Mismatches:   167
Query Match:      8.67%     Indels:      120
DB:                4        Gaps:         20

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US-09-502-945-1 (1-1552) X US-09-538-092-918 (1-1937)

1 CTTCTGATGCATCCGAGAAGCTAAACTTACTTATGAGGAAAGTGTGAATTGAG--- 57

Db 901 LeuAlaAspAlaGluGluArgCysGluGluGluLeuIleLysAsnLysIleGluLeuGluVala

[illegible]

1000

[illegible]

121 AAA-----GAGCACTAAAGCATAAAGAATTCTTCTGCGCTAAT 16

Db 961 GluLeuThrIeuAlaLysValGluLysGluLysHisAlaThrGluAsnLysValLysAsn 988

QY 163 ACTTGTAACCGTGTGGTCTT-----TGTTTGAATGTGCTCAGCATGAAGCT 21

Db 981 LeuThrGluGluMetAlaGlyLeuAspGluThrIleAlaLysLeuSerLysGluLysLys 10

214 GTCTTCCCAACCAIACIAAGIICAIAGCAGACCAI CGAAAGACI BG I AAAAAA 2

[illegible]

$\vdash$

334 AGAGGAAGCAAGTCTTATGAAACAGGTGAACAAGTTTGGCAATATCTGAGGAAGCCAAT 39

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Db      1032 -----GlnGlnValAspAspLeu-----GluGlySer 10
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394 TTGAAAAAACCAAGGCTTAAATCCAGTGTGACCAAGTTGAGGAAGGAGCTGGAGAGGCAG 45

Db 1041 LeuGIuGIuLy-----LyLeuArGMeTAsPLeuGIuArGAla 10

454 GCGAGCGACTTGGAAAAGACTTCGATCTCAGCAAGAGAAAGGCTC--ATGGAGATA 51

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629

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Db      1095 SerLysTlegluAspGluGlnAlaValGluTleglnLeuGlnLysLysIleLysGluLeu 11
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628 ATTCAGCTATTATCACTG---GAGGAATTCAAGCCAGCTGGCTTCTCGGGAATG 688

Db 1115 GlnAlaArgIleGluGluLeuGlyGluGluIleGluAlaGluArgAlaSerArg----- 11

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QY 685 GATGTCAAAAGCTGTGTGGAAATGCGCTATCAGCTGAATAAAACCAATGAGAGAG 744
Db 1133 -----AlaLysAlaGluLysGlnArgSerAspLeuSerArgGluLeu 1146
QY 745 GATGAGCGAAGAAAGGACACAGAGCTTCAAGCAAAAATTAACAGGGATCTTGAATT 804
Db 1147 GlnGluIleSerGluArgLeuGlnGluAlaGlyGlyAlaThrSerAlaGlnValGluLeu 1166
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Db 1167 AsnLysLysArgGluAlaGlnPheGlnLysLeuArgArgAspLeuGlnGluAlaThr-- 1185
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Db 1186 --LeuGlnHisGluAlaMetValAlaIleLeuArgLysHisAlaAspSerMetAla 1204
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QY 976 AGTCAGAAAAAGGTATACATATGATTAATTG----- 1008
Db 1224 LysSerGluLeuLysMetGluThrAspAspLeuSerSerAsnAlaGluAlaIleSerLys 1243
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Db 1263 LysThrLysGlnGlnGlnGlnArgLeuIleAsnAspLeuThrAlaGlnArgAlaArg 1282
QY 1093 -----AGGCAGCTGGAT----- 1104
Db 1283 LeuGlnThrGluAlaGlyGluIleLysArgGlnLeuAspGlnLysAspAlaLeuValSer 1302
QY 1105 -----AAGCAGACGACAGCCACAGCCAGCAGCTGGCAGCTC----- 1143
Db 1303 GlnLeuSerArgSerLysGlnAlaSerThrGlnGlnIleGlnGluLeuLysHisGlnLeu 1322
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QY 1195 GTGGACCGGCTGGGACCCAG 1215
Db 1343 CysAspLeuLeuArgGln 1349
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Search completed: March 12, 2005, 00:41:29  
Job time : 106.912 secs





GenCore version 5.1.6  
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## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 68.6159 Seconds

(Without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-2

Perfect score: 5346  
Sequence: 1 ggaattcccttgcgaagt.....aaacaaaagcttaaaattc 2885

## Scoring table:

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdl  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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## Database :

Issued\_Patents\_AA.\*  
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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4677	87.5	897	4	US-09-849-602-18
2	4560.5	85.3	1114	4	US-09-637-145-4
3	2691	50.3	1041	4	US-09-644-827B-9
4	2691	50.3	1084	4	US-09-637-145-3
5	2691	50.3	1084	4	US-09-538-092-1222
6	1773	33.2	938	4	US-09-637-145-2
7	1739.5	32.5	1200	4	US-09-644-827B-8
8	1739.5	32.5	1428	4	US-09-644-827B-7
9	1573	29.4	706	4	US-09-644-827B-6
10	672	12.6	574	4	US-09-538-092-649
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13	477.5	8.9	386	4	US-09-248-796A-15279	Sequence 15279, A
14	464.5	8.7	141	4	US-09-270-767-33310	Sequence 33310, A
15	447	8.4	630	4	US-09-252-991A-18033	Sequence 18033, A
16	409.5	7.7	387	4	US-09-489-039A-12997	Sequence 12997, A
17	374.5	7.0	335	3	US-09-446-504-80	Sequence 80, Appl
18	374.5	7.0	335	3	US-09-712-266-80	Sequence 80, Appl
19	320.5	6.0	556	4	US-09-949-016-7424	Sequence 7424, Ap
20	310	5.8	444	4	US-09-248-796A-19305	Sequence 19305, A
21	306.5	5.7	465	4	US-09-949-016-10909	Sequence 10909, A
22	306.5	5.7	482	4	US-09-538-092-1308	Sequence 1308, Ap
23	306.5	5.7	482	4	US-08-624-735E-5	Sequence 5, Appl1
24	304	5.7	438	4	US-09-538-092-1367	Sequence 1367, Ap
25	303.5	5.7	433	4	US-08-624-735E-9	Sequence 9, Appl1
26	303.5	5.7	433	4	US-09-645-337A-13	Sequence 13, Appl
27	303	5.7	480	4	US-08-624-735E-10	Sequence 10, Appl
28	302	5.6	482	1	US-08-528-255A-1	Sequence 1, Appl1
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39	275.5	5.1	2088	4	US-09-548-372D-13	Sequence 13, Appl
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## ALIGNMENTS

RESULT 1  
US-09-849-602-18  
Sequence 18, Application US/09849602  
Patent No. 6794501  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Matthew J.  
APPLICANT: Old, Lloyd J.  
APPLICANT: Stockert, Elisabeth  
APPLICANT: Chen, Yao-Tseng  
TITLE OR INVENTION: Colon Cancer Antigen Panel  
FILE REFERENCE: L0461/7105 (JRV)  
CURRENT APPLICATION NUMBER: US/09/849,602  
CURRENT FILING DATE: 2001-05-04  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 18  
LENGTH: 897  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-849-602-18

Alignment Scores:  
Pred. No.: 4.97e-306  
Score: 4677.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 87.49%  
DB: 4  
Gaps: 0

US-09-502-945-2 (1-2885) x US-09-849-602-18 (1-897)

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RESULT 2  
US-09-637-145-4  
Sequence 4: Application US/09637145  
Patent No. 6673587  
GENERAL INFORMATION:  
APPLICANT: EVANS, RONALD M.  
APPLICANT: KAO, HUNG-YING  
APPLICANT: DOMES, MICHAEL  
APPLICANT: ORDENLICH, PETER  
TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR  
FILE REFERENCE: SALK3000  
CURRENT APPLICATION NUMBER: US/09/637,145  
CURRENT FILING DATE: 2000-08-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1114  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-637-145-4

Alignment Scores:  
Pred. No.: 3,546-298 Length: 1114  
Score: 4560.50 Matches: 888  
Percent Similarity: 96.70% Conservative: 19  
Best Local Similarity: 94.67% Mismatches: 25  
Query Match: 85.31% Indels: 7  
Gaps: 2

US-09-502-945-2 (1-2885) x US-09-637-145-4 (1-1114)

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DB 460 SAAA 420  
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DB 480 AA 440  
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DB 500 GAAA 500  
QY 1022 CTACAGCTGGGAGAGCTTCCCAAGAGAGGAGAGCTGCGAGGAGCGGAGCGGAG 1081  
DB 520 MAAA 520  
QY 1082 CTTGAGAGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141  
DB 540 PAAA 540  
QY 1142 CTGACATGCGCGGAGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201  
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QY 1202 GAG 1261  
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QY 1262 GCGAGAGTGTGCTGAGAGAGGAGCGGAGCTTGGAGAGAGCTGAGATCAAAA 1321

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QY      1322 CTGTCTCATGATCCCAACCGCTGCAACCTTTGCAGGTGTACCAAGCGCCCTCAGGCTG 1381
Db      619 LeuPheAlaMetAlaGlnGlnLeuGlnProLeuGlnValTyrGlnAlaProLeuSerLeu 638
QY      1382 GCCACGTGTG-CCCAACCAAGCCCTGGGCGGTACCCCAATCTTCCTGCTGCTGGGGGCG 1441
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Db      659 MetLysSerProThrAspGlnProThrValValLysHisLeuPheThrThrGlyValVal 678
QY      1496 TACGACACGTTTACGTAAAGACACAGTGCATGTGCGGGAACAACAAGTGCACCTGAG 1555
Db      679 TyrAspThrLeuMetLeuLysHisGlnCysMetCysGlyLysThrHisValHisProGlu 698
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Db      699 HisAlaGlyAryGlnGlnSerIleTrpSerArgLeuGlnGlnThrGlyLeuLeuGlyLys 718
QY      1616 TGGAGCGGATCCGAGGCTGGCAAAAGCCAGCTGATGATGATCCAGACAGTGCACCTCGAA 1675
Db      719 CysGlnThrGlnLeuArgGlyArgLysAlaThrLeuAspGlnIleGlnThrValHisSerGlu 738
QY      1676 TACCAACACCTTCTCTATGGAGCAGTCCCTCAACCGGCAAGAAGTACAGCAAGAAG 1735
Db      739 TyrHisThrLeuLeuTyrGlyThrSerProLeuHisThrGlnLysLeuAspSerLysLys 758
QY      1736 TTGCTGGGTCCCATCAGCCAGAAAGATGTATGCTGTGCTGCTGCTGGGGGCATCGGGGTG 1795
Db      759 LeuLeuGlyPrcIleSerGlnLysMetTyrAlaMetLeuProCysGlyGlyIleGlyVal 1778
QY      1796 GACAGTGACACCGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1855
Db      779 AspSerAspThrValTrpAsnGlnMetHisSerSerSerAlaValAlaGlyMetAlaValGly 798
QY      1856 TGCCTGTGAGATGAGCTTCAAGGTGCTGCAAGAGAGCTCAAGATGATGATGATGATGATGATG 1915
Db      799 CysLeuValGlnLeuAlaPheLysValAlaAlaGlyLysLeuLysAsnGlyPheAlaIle 818
QY      1916 ATCCGGCCCCCAGACAGACCGCCGAGGATCCACAGCCATGGGATCTGCTTCTTCAAC 1975
Db      819 IleArgProProGlyHisHisAlaGlnGlnSerThrAlaMetGlyPheCysPhePheAsn 838
QY      1976 TCTGTGACCATCA-CCGCAAACTCCTACAGACAGATGTAACGATGGGCAAGGCTCATC 2035
Db      839 SerValAlaIleThrAlaLysLeuLeuGlnGlnLysLeuSerValGlyLysValLeuIle 858
QY      2036 GTGAGCTGGACATTCACATGCAATGCAATGCAACCGACGCGCTTCTTCAATGACCCCTCT 2095
Db      859 ValAspTrpAspIleHisHisGlyAsnGlyThrGlnIleAlaPheTyrAlaAspProSer 878
QY      2096 GTGCTCTACATCTCTGTCATCCGCTATGACAGAGGAACTTTTCCAGGCTCTGGGCT 2155
Db      879 ValLeuTyrLleSerLeuHisArgTyrAspAsnGlyAsnPhePheProGlySerGlyAla 898
QY      2156 CCGAAGAGGTTGGTGGAGACAGCGGTGGGGATCAATGTAACGTTGGATGGACAGCA 2215
Db      899 ProGlnGlnValGlyGlyLysProGlyValGlyTyrAsnValAsnValAlaIleProGly 918
QY      2216 GGTGTGAGACCCCATTTGAGACGTGAGATCCTTACAGCTTCAAGACAGTGTGATG 2275
Db      919 GlyValAspProProCileGlyAspValGlyLysLeuThrAlaPheArgThrValValMet 938
QY      2276 CCGATTGCCACAGATTTCTACCTGATGTGCTCTTATCTCCGCGGGGTTGATGCTGTT 2335
Db      939 ProIleAlaGlnGlnLysHisSerProAspValValLeuValSerAlaGlyPheAspAlaVal 958
QY      2336 GAAGGACATCGTCTCTCTGGGGGTGCTACTGCTGACCGGCAAGTGTGTCACATG 2395
Db      959 GlnGlyHisLeuSerProLeuGlyGlyTyrSerValThrAlaArgCysPheGlyHisLeu 978

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QY      2396 ACCAGGACCTGATGATCCCTGGAGGGGCGCGGTGCTGCTGAGCCCTGAGGAGGCAAT 2455
Db      979 ThrArgGlnLeuMetThrLeuAlaGlyArgValValLeuAlaLeuGlnGlyGlyHis 998
QY      2456 GACTTGAACCGCATCTGTATGATGCTTCTGAAAGCTGTGTGCTGCTGCTGCTGCTGCTG 2515
Db      999 AspLeuThrAlaIleCysAspAlaSerGlnAlaCysValSerAlaLeuLeuSerValGlu 1018
QY      2516 CTGACACCTTGGATGAGCAGTCTTGCAGCAAAAGCCCAACATCAACAGTGGCCAG 2575
Db      1019 LeuGlnProLeuAspGlnAlaValLeuGlnGlnLysProSerValAsnAlaValAlaThr 1038
QY      2576 CTAGAGAAATCATCATGATTCAGACAGAAACACTGAGCTGTGTGCAAGATTGCGCGCT 2635
Db      1039 LeuGlnLysValIleGlnIleGlnSerLysHisTrpSerCysValGlnArgPheAlaIle 1058
QY      2636 GCTCTGGCCCGGCTGCTGCTGAGAGGGCCCAAGCAGTGGACCGAAGACCGAAT-GrG 2694
Db      1059 GlyLeuGlyCysSerLeuArgGlnAlaGlnThrGlyLysLeuGlnAlaGlnThrVal 1078
QY      2695 AACGCCATGAGCTTGTGCTGAGGGGCGCAAGAGCCCAAGCTGCGCAGCCGCGAA 2754
Db      1079 SerAlaMetAlaLeuLeuSerValGlyAlaGlnGlnAlaGlnAlaValAlaThrGlnGlu 1098
QY      2755 CACAGCCCCAGCGCGGACAGAGAGCCATGAGACAGAGACCTGCGCTG 2802
Db      1099 HisSerProArgProAlaGlnGlnProMetGlnGlnGlnProAlaLeu 1114

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## RESULT 3

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US-09-644-827B-9
; Sequence 9, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644,827B
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-9

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## Alignment Scores:

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Pred. No.: 1,27e-172 Length: 1041
Score: 2691.00 Matches: 568
Percent Similarity: 71.38% Conservative: 118
Best Local Similarity: 59.11% Mismatches: 195
Query Match: 50.34% Indels: 81
DB: 4 Gaps: 23

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US-09-502-945-2 (1-2885) x US-09-644-827B-9 (1-1041)

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QY      2 GAATTCCTCTGTGCGAATCAAGAGCCACAGCGGCGCTCAACATTCCTCCCA 61
Db      134 GlnPheValLeuAsnLysLysLysAlaLeuAlaHisArgAsnLeuHisHisCysIleSer 153
QY      62 CAGCACCCTCAATGCTG-----GGAGCCACCATGCTTTCTTGGACCAAGATTCCCT 115
Db      154 SerAspProArgTyrTrpTyrGlyLysThrGlnHisSerSerLeuAspGlnSerSerPro 173
QY      116 CCCCAGAGGGGCGCCCTGGAGCGCTCCCTCTTAACAACTGCTTGTGCTGGGCGCTTAC 175

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Db 174 ProGlnSer-----GlyValSerThrSerTyraHisProValLeuGlyMetTyr 190  
Qy 176 GACAGTGAAGACGATTCCCGCTCGGAAAACAGCTCTGAACCAATTGAAGTGGT 235  
Db 191 AspAlaIuysAspAspPheProLeuArgIuysThrAlaSerGluProAsnLeuIuysArg 210  
Qy 236 TCAGAGCTAAACAGAAAGTGGCTGAGCGGAGAAAGCATCCCTCTCGCTGCGAAGAT 295  
Db 211 SerArgLeuIuysGlnValAlaGluArgHisSerSerProLeuLeuArgIuysAsp 230  
Qy 296 GGAAGCTGTATTAGACCTTTAAGAAGAGCTTTGAGATCAGAGTGGCCGGGCTGGG 355  
Db 231 GlyProValIuysThrAlaLeuIuysValArgProLeuAspValIuys----- 245  
Qy 356 GCGTCGTCGCTGTAACAGGACCGGCTCGGCGCCAGCTCTCC---AAGAGCTCC 412  
Db 246 ---AspSerAlaCysSerSerAlaProGlySerGlyProSerSerProAsnAspSerSer 264  
Qy 413 CACAGACCATCGCTGGAATGCTTTACTGGCTCAGTCCCAATCCCAATCCCACTGAGATG 472  
Db 265 GlySerAlaSerAlaGluAsnGlyIleAlaProAlaAlaProSerIleProAlaGluThr 284  
Qy 473 CTCCTCAGACCGAGCCCTCTCTGAGACGCTCCCAACCAAGTTCAAGCTTCAACG 532  
Db 285 SerLeuAlaHisArgLeuValAlaArgGluGlySerAlaAlaProLeuProLeuTyrThr 304  
Qy 533 TTCCTCTCTGCGCAATCTCTCGTGGGTGAGCGCAACGGTCACCTGTCAACCACTCA 592  
Db 305 SerProSerLeuProAsnIleThrLeuGluIuysProAlaThr----- 318  
Qy 593 CACCTCAGCTGCTCCCGAAGCTGTGACA-----CAGCAGAGGCGGAGAGCAGGCC 646  
Db 319 -----GlyProSerAlaGlyThrAlaGlyGlnGlnAspThrGluArgLeuThr 334  
Qy 647 CTCAGTCCCTCGGCGGAG-----GATGACAGCTGACCGGCACTTCATG 691  
Db 335 LeuProAlaLeuGlnGlnIuysArgSerLeuPheProGlyThrHisIuysLeuThrProTyrLeu 354  
Qy 692 AGCAATCTCTATTCTGCTGCTGCTGCGCTGAGCGGCGAGCGGAGCGGAGCGCC 751  
Db 355 SerThrSer-----ProLeuGluIuysArgGlyAla 365  
Qy 752 CACGAGCAGCTCTCTGCTGAGCATGTGCTGTGCTGAGCAGCGCCGAGCAGACAG 811  
Db 366 ---AlaHisSerProLeuLeuGlnHisMetValLeuLeuGluGlnProProAlaGlnAla 384  
Qy 812 ACCCTCATT-----GCTGTGCACTCCAGCGGCACTCCCACTAGTGAAGGAGT 859  
Db 385 ProLeuValIuysArgIuysAlaLeuProLeuHisAlaGlnSer---LeuValGlyAla 403  
Qy 860 GAACGTGTGGCCACACATGCGGACGAGTGAAGCAAGTCCCGCGGCACTCGGCGCTGAGC 919  
Db 404 AspArgValSerProSer-----IleHisValuysLeuArgGlnHisAspArgProLeuGly 420  
Qy 920 CGCACTAGTCTCTCAGCTGCGGCGGAGATCCCGAGGCGCTGAGCAGCTGATCAAG 979  
Db 421 ArgThrGlnSerAlaProLeuProGlnAspAlaGlnAlaLeuGlnHisIuysValAlaIleGln 440  
Qy 980 CAACAGACACAGAGTTCTGTGAAGACAGAG-----CAGCAGCAGCTTACAG 1027  
Db 441 GlnGlnHisGlnGlnPheLeuGlnIuysHisIuysGlnGlnPheGlnGlnGlnGln 460  
Qy 1028 CTGGGCAAGATCTCCACCAAGACAGGAGAGTCCCGAGCGGACCCACCACTCCAG 1087  
Db 461 MetAsnIuysAlaIleProIuysProSerGluProAlaArgIuysProGluIuysArgProGlu 480  
Qy 1088 GAGACAGAGAGAGTGAAGAGAGTGAAGAGTCTTGTGAGGAGAGAGAGAGAGAGAGAG 1144  
Db 481 GlnThrGlnIuysGlnIuysValuysArgGlnHisGln---AlaLeuLeuAspArgIuysProTyrLeuAsp 499  
Qy 1145 ACCATGCGCGGAGGAGCTCCACAGAGTGAAGACACACAGAGAGCTGAGAGAGAG 1204  
Db 500 ArgLeuProGluIuysGlnIuysAlaHisAlaGlnIuysAlaGln---ValIuysGlnGln 518

Qy 1205 GACGAGAGAGAGTGGGAGAGAGAGAGATTCATCCAGGTTAAGACGAGAGGCG 1264  
Db 519 ProIleGlnSerAspArgGlnGlnAlaGln-----ProProArgGlnVal 533  
Qy 1265 GAGAGTGTCTGACAGAGGCGCGGACTTGAAGAGCTGTGTGTGATACAAAATCG 1324  
Db 534 GluProGlyIuysArgGln---ProSerGlnGlnGlnIuysLeuPheArgGlnAlaLeu 552  
Qy 1325 TTCCTCAGATCCCAACCGCTGCAACCTTTCAGAGTGAACCAAGCGCCCTCAGCTGGCC 1384  
Db 553 LeuLeuGlnGlnGlnArgIleHisGlnLeuAspAsnTyrGlnAlaSerMetGlnAlaAla 572  
Qy 1385 ACTGTGCCC-----CACCAAGCTCGGCGGCTGACCCCAATCTCCCTGCT 1429  
Db 573 GlyIleProValSerPheGlnGlyHisArgProLeuSerArgAlaGlnSerSerProAla 592  
Qy 1430 GCC-----CTGGGAGGATGAAGAACCCCGCAGACCAACCGCTCAAGACCTTTC 1480  
Db 593 SerAlaThrPheProValSerValGlnGluProProThrIuysPro-----ArgPhe 609  
Qy 1481 ACCACAGTGTGCTTACGACACGTTCACTATGCTAAAGCACAGTGCATGTGCGGAAACA 1540  
Db 610 ThrThrGlyLeuValIuysArgThrLeuMetLeuHisGlnCysThrCysGlySerSer 629  
Qy 1541 CAGGTGCACTGAGCATGTGCGCGGATCCAGAGCATCTGTCTCGGCTGCGAGAGACA 1600  
Db 630 SerSerHisProGlnHisAlaGlyArgIleGlnSerIleThrSerArgLeuGlnIuysThr 649  
Qy 1601 GGCCTGTGTAAGACGTGCGAGCGGATCCGAGGTGCGAAGCCAGCTAGATGATCAG 1660  
Db 650 GlyLeuArgGlyIuysCysGlnCysIleArgGlyArgGlyValThrLeuGlnGlnLeuGln 669  
Qy 1661 ACAGTGCATCTGAATACACACCTGCTTAAAGGACAGCATCCCTCGCAACCGGCAAG 1720  
Db 670 ThrValHisSerGlnIuysAlaHisThrLeuIuysGlyThrAsnProLeuAsnArgGlnIuys 689  
Qy 1721 CTAGACAGCAAGAGTTGCTCGGCTCCATCAGCAGAGATGATGCTGTGCTGCTTGT 1780  
Db 690 LeuAspSerIuysIuysLeuLeuGlySerLeuAla---SerAlaPheValArgLeuProCys 708  
Qy 1781 GGGGCGCATCGGGGTGACACTGACACCTGTGTGAATGAATGACATCTCTCAGTCTGTG 1840  
Db 709 GlyGlyValGlyValAspSerAspThrIleTyrAsnGluValHisSerAlaGlyAlaAla 728  
Qy 1841 CGCATGCGAGTGGGCTGCTGCTGAGCTGAGCTTCAAGTGGCTGAGAGAGCTCAAG 1900  
Db 729 ArgLeuAlaValGlyCysValAlaGluLeuValPheIuysValAlaThrGlyIuysLeuIuys 748  
Qy 1901 AATGGAATTTGCAATCCGCGCCCGGAGCAGCAGCAGCGGAGGATCCACAGCGCATGGA 1960  
Db 749 AsnGlyPheAlaValAlaIuysProProGluHisHisAlaGlnIuysThrProMetGly 768  
Qy 1961 TTCTGCTTCTTCACTGTAGCCATCAGCGCAAACTCTTACAGCAAGATTGAAGTGTG 2020  
Db 769 PheCysTyrPheAsnSerValAlaValAlaIuysLeuLeuGlnGlnArgLeuSerVal 788  
Qy 2021 GCGAAGCTCTCATCTGGACTGGACATTCACATTCAGGCAATGGCAGCAGCGGCTTC 2080  
Db 789 SerIuysIleLeuIleValAspTyrAspValHisHisGlyAsnHisIuysThrGlnIuysAlaPhe 808  
Qy 2081 TACAAAGACCCCTGAGCTCTACATCTCTGATCCGATGATGACAAAGGGAATCTTT 2140  
Db 809 TyrSerAspProSerValLeuIuysTyrMetSerLeuHisArgTyrAspArgIuysAspPhePhe 828  
Qy 2141 CAGAGCTGTGGGCTCTGAAGAGTGTGTGAAGACAGGCGTGGGATCAATGTGAAC 2200  
Db 829 ProGlySerGlyAlaThrAspArgIuysAlaGlyThrGlyProGlyValGlyPheAsnValAsn 848  
Qy 2201 GTGCAATGACAGAGAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2260  
Db 849 MetAlaPheThrGlyIuysLeuAspProProMetGlyAspAlaGlnIuysThrAlaAlaPhe 868

QY 2261 AGGACAGTGTGATGCCATTGCCACGAGTTCTACCTGATGTCCTAGTCTCGCC 2320  
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Db ArgThrValValMetProIleLeuSerGlnPheAlaProAspValValIleuValSerSer 888  
QY 2321 GGGTTTGAACGCTGTGAAGACATCTGTCTCTCTGCTGCTGCTACTCTGACCCGCCA 2380  
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Db GlyPheAspAlaValGlnGlnHisProThrProIleuGlyGlyTrpLeuSerAlaArg 908  
QY 2381 TGTGTTGGCAGCTTACACGAGGAGCTGATGACCTGGCAGAGGAGCCGGGTGCTGGCC 2440  
|||  
Db CysPheGlyTrpLeuThrTrpGlnIleuMetGlyLeuAlaGlyAlaGlyIleValIleuAla 928  
QY 2441 CTGAGGAGGAGGACCTGATGACCTGACCGCATGTGATGCTCTGAGCTTGTCTGCTGCT 2500  
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Db LeuGlnGlyTrpHisAspLeuThrAlaIleCysAspAlaSerGlnAlaCysValSerAla 948  
QY 2501 CTGCTCAGTTAAAGCTGACGAGCCCTTGGATGAGGACGCTTTCAGCAAAAGCCCAATC 2560  
|||  
Db LeuLeuGlyTrpAsnGluLeuAspProLeuProGlnIleuValIleuGlnIleuArgProAsnAla 968  
QY 2561 AACGAGTGGCCACGCTAGAGAAAGTCATCGAGATCCAGCAAAAGCTGAGCTGTGTG 2620  
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Db AsnAlaValAlaArgSerMetGlnIleuValMetGlnIleuHisSerTrpTrpArgCysLeu 988  
QY 2621 CAGAGTTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2680  
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Db GlnArgThrTrpSerThrAlaGlyArgSerIleuIleGlnIleuThrCysGlnAsnGln 1008  
QY 2681 GAAGCCGCAAT-GTGAAGCCGCAATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2739  
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Db 1009 GlnAlaGlnThrValThrAlaMetAlaSerLeuSerValGlyValIleuProAlaGln 1027  
QY 2740 GCGGACGCGCGAGAACACAGCCCGGACGCGGACGCGGACGCGGACGCGGACGCGG 2799  
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Db 1028 -----LysArgProAspGlnIleuProMetGlnIleuProPro 1040  
QY 2800 CTG 2802  
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Db 1041 Leu 1041

RESULT 4  
US-09-637-145-3  
; Sequence 3, Application US/09637145  
; Patent No. 6673587  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; APPLICANT: KAO, HUNG-YING  
; APPLICANT: DOMNES, MICHAEL  
; APPLICANT: ORDENTLICH, PETER  
; TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR  
; FILE REFERENCE: SLK3000  
; CURRENT APPLICATION NUMBER: US/09/637,145  
; CURRENT FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1084  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-637-145-3

Alignment Scores:  
Pred. No.: 1,284-172 Length: 1084  
Score: 2691.00 Matches: 568  
Percent Similarity: 71.36% Conserves: 118  
Best Local Similarity: 59.11% Mismatches: 195  
Query Match: 50.34% Indels: 81  
Gaps: 23

US-09-502-945-2 (1-2885) x US-09-637-145-3 (1-1084)  
QY 2 GAATTCCTTTGTAAGTCAAGAGACCCACACAGCGGCTCAACATTCCTCCCA 61  
|||||:|||||:|||||  
|||||:|||||:|||||

Db 177 GluPheValIleuAsnIleuValAlaLeuAlaHisAlaAsnIleuAsnHisCysValSer 196  
QY 62 CAGACACCCCAATGCTG-----GGAGCCACCATGCTTTTGGACGAGATTCCTCC 115  
|||  
Db 197 SerAspProArgTrpTrpArgGlySerThrGlnHisSerSerLeuAsnSerPro 216  
QY 116 CCCCAGAGCGGCCCCCTGGAGCGCTCCCTCCCAACATGCTTGGCTGGGCCCC 175  
|||  
Db 217 ProGlnSer-----GlyValSerThrSerTrpAsnHisProValIleuGlyMetTrp 233  
QY 176 CAGAGTCGAGAGCACTTCCCTCCGCAAAAGCCTCGAAGCCCACTGAAGTGGCT 235  
|||  
Db 234 AspAlaLeuAspAspPheProLeuArgGlySerAlaSerGlnProAsnIleuValAsp 253  
QY 236 TCAGGCTTAAACAGAAAGTGGCTGAGCGGAGAGAGTCCCTCTGCTGCTGCAAGAT 295  
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Db 254 SerArgLeuIleuGlnIleuValAlaGlnIleuGlnArgSerProLeuLeuArgTrpValAsp 273  
QY 296 GGGACTGTATTAGACCTTTAAGAAAGAGCTGTGAATCAACAGTCCGGGCTGGG 355  
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Db 274 GlyProValIleuThrAlaLeuIleuValAspArgProLeuAspValThr----- 288  
QY 356 GCGTCCTCCGCTGTAAACAGCGGACCGGCTCCGGCCAGCTTCC---AAGAGTCC 412  
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Db 289 ---AspSerAlaCysSerSerAlaProGlySerGlyProSerSerProAsnHisSer 307  
QY 413 CACGACACCATGCTGAGATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472  
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Db 308 GlySerValSerAlaGlnAsnGlyIleAlaProAlaValProSerIleProAlaGlnThr 327  
QY 473 CTCCCTCAGACCGGACCTCCCTCTGACAGCTCCCAACAGTCAAGCTTACAG 532  
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Db 328 SerLeuAlaHisArgLeuValAlaArgGlnGlySerAlaAlaProLeuProLeuTrp 347  
QY 533 TCTCCTTCTTCTGCGCAACATCTCCCTGAGGCTGACGCGGACGCTGCTGCTGCTGCTGCTGCT 592  
|||  
Db 348 SerProSerLeuProAsnIleuThrLeuGlyLeuProAlaThr----- 361  
QY 593 CACCTCAGTCCCTCCCGAAGCTGTGACA-----CAGCAGAGGCGGAGGAGGCGG 646  
|||  
Db 362 -----GlyProSerAlaGlyThrAlaGlyGlnIleuAspThrGlnThr 377  
QY 647 CTCAGTCCCTGCGGAG-----GTTGCAAGCTGACCGGCAATTCATG 691  
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Db 378 LeuProAlaIleuGlnIleuArgLeuSerLeuPheProGlyThrHisIleuThrProTrpLeu 397  
QY 692 AGCAGATCCCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751  
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Db 398 SerThrSer-----ProLeuGlnIleuArgAspGlyAla 408  
QY 752 CAGGCGATGCTCCCTGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811  
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Db 409 ---AlaHisSerProLeuLeuGlnIleuMetValIleuLeuGlnIleuProAlaGlnAla 427  
QY 812 ACCCTCATT-----GCTGTCACCTTCACGCGAGTCCCACTAGTACGGGT 859  
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Db 428 ProLeuValThrGlyLeuGlnAlaLeuProLeuHisAlaGlnSer---LeuValGlyAla 446  
QY 860 GAACGTGTGGCCACGACATGCGGAGGTAGAGAAAGTCCCGGAGATGGGCGGCGGAGC 919  
|||  
Db 447 AspArgValSerProSer-----IleHisIleuArgGlnIleuHisArgProLeuGly 463  
QY 920 CGACATCAGTCCCTCAGCGCTGCGGACAGTCCCGGAGGCTTGGACGAGTGTATGCA 979  
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Db 464 ArgThrGlnSerAlaProLeuProGlnIleuAlaGlnAlaIleuGlnIleuValIleuGln 483  
QY 980 CAAACACACGAGGATTCCTGAGAAAGAG-----CAGCAGCAGTACAG 1027  
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Db 484 GlnGlnHisGlnIleuPheLeuGlnIleuValHisIleuGlnIleuPheGlnIleuGlnIleuGln 503  
QY 1028 CTGAGCAAGATCTTCAACAGAGAGGAGGAGTCCCGGAGGAGGCGGACGCGGCTGAG 1087  
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Db 504 MetAsnIleuIleuProIleuProIleuProIleuProIleuProIleuProIleuProIleuProIleu 523





US-09-538-092-1222

## Alignment Scores:

Prod. No.:	1,28e-172	Length:	1084
Score:	2591.00	Matches:	568
Percent Similarity:	71.38%	Conservative:	118
Best Local Similarity:	53.11%	Mismatches:	195
Query Match:	50.34%	Indels:	81
DB:	4	Gaps:	23

US-09-502-945-2 (1-2885) X US-09-538-092-1222 (1-1084)

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QY 2 GAATTCCTTTCGAAATCAAGAGCCCAACAGCGCGCTCAACATTCCTCCCA 61
Db 177 GluPheValLeuAenlyslYsAlaLeuAlaHisArgAsnLeuAenHisCysIleSer 136
QY 62 CAGACCCCAAAAGCTGG-----GGAAGCCACCATGCTTCTTGGACGAGATTCCTT 115
Db 197 SerAspProArgTyrTyrGlyTyrGlnHisSerSerLeuAspGlnSerPro 216
QY 116 CCCGAGAGCGGC-CGCCCTGGAGCGCTCCCTCTCAAAATGCGCTTGGCGGCGCTAC 175
Db 217 ProGlnSer-----GlyValSerThrSerThrAsnHisProValIleuGlyMetTyr 233
QY 176 GACAGTCGAGACACTTCCCTCCGCAAAACAGCCTTGAACCACTTGAAGTGCCT 235
Db 234 AspAlaIysAspAspPheProLeuArgTyrThrAlaSerGluProAenLeuYsleuArg 253
QY 236 TCAGAGCTTAAATAGAAAGTGGCTGAGCGGAGAAAGCATGCTCCCTCGCTGCCAAGAT 235
Db 254 SerArgLeuYsGlnYsValAlaGluArgSerSerProLeuLeuArgTyrAsp 273
QY 296 GGACAGCTTATAGACCTTAAAGAGAGAGCTTGAATGATCAAGGTGCGGCGCTGGG 355
Db 274 GlyProValValThrAlaLeuYsYsArgProLeuAspValThr----- 288
QY 356 GCGCTGCTCGGTATTAACAGCGCACCGGCTCGGCGCCAGCTCTGCC--AAAGCTCC 412
Db 289 ---AspSerIaCysSerSerAlaProGlySerGlyProSerSerProAenAsnSerSer 307
QY 413 CACAGCACCATCGTGAAGATGCTTACTGCTCACTGCCCAACATCCCACTGAGATG 472
Db 308 GlySerValSerIaGlnAenGlyIleAlaProAlaValProSerIleProAlaGluThr 327
QY 473 CTCCTCAGACGAGCGCTCCCTCTGACAGCTCCCAACAGTTCAGCTCTACAG 532
Db 328 SerLeuAlaHisArgLeuValAlaArgGluGlySerAlaAlaProLeuProLeuTyrThr 347
QY 533 TCTCTTCTGCTCCCAACATCTCCCTAGGCTGCAAGGCCAAGCTCACTGCACCAACTCA 592
Db 348 SerProSerLeuProAenIleThrLeuGlyLeuProAlaThr----- 361
QY 593 CACCTCACTGCTCCCGGAAGCTGTGACA-----CAGCAGAGAGCCGAGAGAGGCC 646
Db 362 -----GlyProSerAlaGlyThrAlaGlyGlnGlnAspThrGluArgLeuThr 377
QY 647 CTCAGATCCCTGCKCKAG-----GGTGCACGCTGACCGGCAAGTTTCATG 691
Db 378 LeuProAlaLeuGlnArgLeuSerLeuPheProGlyThrHisIleuThrProTyrLeu 397
QY 692 AGCAGCATCTCTATTCTTGCTGCTGCTGAGGCTGAGGCTGAGAGGCGAGAGCCCC 751
Db 398 SerThrSer-----ProLeuGlnArgAspGlyAla 408
QY 752 CAGGGGATGCGCTCCCTGCTGACATGCTGTGCTGAGACAGGCGCGGACAGAGC 811
Db 409 ---AlaHisSerPro-LeuLeuGlnHisMetValLeuLeuGlnInProProAlaGlnAla 427
QY 812 ACCCTCAT-----GCTGTGCACTCCACGCGGAGTCCCACTAGTGAAGCGGT 859
Db 428 ProLeuValThrArgLeuGlyAlaLeuProLeuHisIaIaGlnSer---LeuValGlyAla 446
QY 860 GAAAGTGTGCGCACGCGATGCGGACGGTAGGCAAGCTCCCGCGGCACTCGGCGCTGAGC 919

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Db 447 AspArgValSerProSer-----IleHisYsYsLeuArgGlnHisArgProLeuGly 463
QY 920 CGCAGCTCAGTCCCTCGAGCTGCGGAGAGATCCCGAGCGCCCTGAGAGCTGATGACA 979
Db 464 ArgThrGlnSerAlaProLeuProGlnAsnAlaGlnAlaLeuGlnHisIleuValIleGln 483
QY 980 CAAACAGCACAGCAGTTCCTGAGAAAGAGAG-----CAGACAGCTTACAG 1027
Db 484 GlnGlnHisGlnInPheLeuGlnYsHisYsGlnGlnInPheGlnGlnInGlnInLeuGln 503
QY 1028 CTGGGCAAGATCTTCAACCAAGACAGGAGCTGCGGAGCGGCGCCACACCCCTGAG 1087
Db 504 MetAsnIlyIleIleProYsProSerGluProAlaArgGlnProGluSerHisProGlu 523
QY 1088 GAGACAGAGAGAGAGCTGACGAGAGAGAGAGTCTTCTGGGAGGAGGAGCGCTG--- 1144
Db 524 GluThrGlnGlnInLeuLeuArgGlnHisGln---AlaLeuLeuAspGluProTyrIleuAsp 542
QY 1145 ACCATGCCCGGAGGAGCTCCACAGAGAGTGAAGACACAGAGAGCTGAGAGAGAG 1204
Db 543 ArgLeuProGlyGlnYsGlnAlaHisIaIaGlnAlaGlyValGln---ValYsGlnGln 561
QY 1205 GACAGAAAGAGATGGGAGAGAGAGAGATTCATCCAGTTAAAGACAGAGGCGC 1264
Db 562 ProIleGlnSerAspGlnGlnGlnAlaGlu-----ProProArgGlnVal 576
QY 1265 GAGAGTGTGTGAGAGAGGAGGCGCGCATGAGAGAGCTGAGTGCATTAACAAAACAG 1324
Db 577 GluProGlyGlnArgGln---ProSerGlnGlnInLeuLeuPheArgGlnGlnAlaLeu 595
QY 1325 TTCTCAGATGCCCAACCGCTGCAACCTTTCAGAGTGAACCAAGCGCCCTCAGCGTGC 1384
Db 596 LeuLeuGlnGlnInArgIleHisGlnInLeuArgAsnTyrGlnHisSerMetGlnAlaIa 615
QY 1385 ACTGTGCC-----CACCAAGCCTTGGCGCGTACCCCAATCTCCCTGCT 1429
Db 616 GlyIleProValSerPheGlyGlyHisArgProLeuSerArgAlaGlnSerProAla 635
QY 1430 GCC-----CCTGGGAGCATGAAGAACCCCGGACCAACCCGCTCAAGCACTCTTC 1480
Db 636 SerAlaThrPheProAlaSerValGlnGluProProThrIlyPro-----ArgPhe 652
QY 1481 ACCCAAGTGTGTGCTTACACACATTCATGCTTAAAGACACAGTGCATGTGGGAAACACA 1540
Db 653 ThrThrGlyLeuValYsAspThrIleuMetLeuYHisGlnCysThrCysGlySerSer 672
QY 1541 CAGCTGCACCTGAGACATGCTGCGCCGATCCAGAGCATCTGTGCTCCGCTGACAGAGACA 1600
Db 673 SerSerHisProGlnHisIaGlyArgIleGlnSerIleTrpSerArgLeuGlnGluThr 692
QY 1601 GGCCTGCTTAAAGCAAGTGCAGGAGGATCCGAGGTCGCAAGGCCAGCTGATGATCCAG 1660
Db 693 GlyLeuArgGlyYsYsCysGlnCysIleArgGlyArgYsYsAlaThrLeuGlnGlnLeuGln 712
QY 1661 ACAATGCACTTGAATATACACACCTCTGTATGAGACAGATCCCTCAACCGGCAAG 1720
Db 713 ThrValHisSerGlnAlaHisThrIleuLeuYrGlyThrAsnProLeuAenArgGlnYs 732
QY 1721 CTAGACAGCAAGAGTTGCTCGGCTCCCATCAGCAGAAAGATGATGCTGCTGCTTGT 1780
Db 733 LeuAspSerIlyYsYsLeuLeuGlnYsSerLeuAla---SerValPheValArgLeuProCys 751
QY 1781 GGGGAGATGGGGGTGACAGTGCACAGTGTGAATGATGATGACCTCCAGTGCCTGAG 1840
Db 752 GlyGlyValGlyValAspSerAspThrIleTrpAspGlnValHisSerAlaGlyAlaIa 771
QY 1841 CGCATGAGAGATGGGCTGCTGCTGAGATGCTGAGCTTCAAGGTGCTCAGAGAGCTCAAG 1900
Db 772 ArgLeuAlaValGlyYsValValGlnLeuValPheYsValAlaThrArgGlnLeuYs 791
QY 1901 AATGATTTTGCACTATCCGCGCCCAAGACACACGCGGAGGAATCCACAGCATGGA 1960

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Db      792  AaaglyPheAlaValValArgProProGlyIhNhiShiAlaGluGluSerThrProMetGly  811
Qy      1961  TTGTGCTCTTCAACTCTGTAGCCATCAACCCGAAATCTCTACAGCAGAGATTGAAGCTG  2020
Db      812  PheCytyrPheAaSerValAlaValAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  831
Qy      2021  GGCAAGGCTCATATGTCAGCATGGGAGCAATTGACCAATGGCAATGGCAACGAGCGCTTC  2080
Db      832  SerIySIIleuIIleuIIleuIIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  851
Qy      2081  TACAATGACCCCTGTGTCTCTACATCTCTGTGATCGCTGATAGCAAGCGGAACTTCTTT  2140
Db      852  TySerIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  871
Qy      2141  CGAGGCTCTGGAGGCTCTGAAAGAGTTGATGAGAGCAGGCGTGGAGGATCAATGTGAAC  2200
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Db      912  ArgIhIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  931
Qy      2321  GGGTTTATGCTGTGTAAGACATCTGTCTCTCTGTGGTGGCTACTCTGTACACCGCAGA  2380
Db      932  GlyPheAaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  951
Qy      2381  TGTTTTGGCCACTTGACACGAGCTATAGACCTTGGAGGGGGCGGGGTGTGTGGCC  2440
Db      952  CySPheGlyTyLeuThrIyLeuGlyIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  971
Qy      2441  CTGGAGGAGGAGCAATGACTTGACCGGCATCTGTGATGCTGTGAGAGCTTGTGTGGCT  2500
Db      972  LeuGluGlyGlyIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  991
Qy      2501  CTGCTCACTGTAAAGCTTGACAGCCCTTGGATGAGGCGAGTCTTGACAGCAAAAGCCCAATC  2560
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Qy      2561  AAGCAGTGGCCAGCGTGAAGAAAGTCAATCGATCCAGAGCAAACTGAGCTGTGTG  2620
Db      1012  AaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  1031
Qy      2621  CAGAAGTTCGGCGCTGCTGTGGCGCGGCTCTGCGAGGGGGCCAAAGCGAGAGACGGA  2680
Db      1032  GlnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  1051
Qy      2681  GAAGCCGGAAT-GTGAAGCGCATGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  2739
Db      1052  GlnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  1070
Qy      2740  GCGGCAAGCCCGGGAACACAGCCCGGCGGAGAGAGAGCCCATGAGACAGAGCTTGC  2799
Db      1071  -----LyaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa  1083
Qy      2800  CTG 2802
Db      1084  Leu 1084

RESULT 6
US-09-637-145-2
; Sequence 2, Application US/09637145
; Patent No. 6673587
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: KAO, HUNG-YING
; APPLICANT: DOWNS, MICHAEL
; APPLICANT: ORDENTLICH, PETER
; TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR
; FILE REFERENCE: SAKK3000

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CURRENT APPLICATION NUMBER: US/09/637,145
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-637-145-2

Alignment Scores:
Pred. No.: 5,59e-111 Length: 938
Score: 1773.00 Matches: 422
Percent Similarity: 54.79% Conservative: 110
Best Local Similarity: 43.46% Mismatch: 250
Query Match: 33.16% Indels: 190
DB: 4 Gaps: 24

US-09-502-945-2 (1-2885) x US-09-637-145-2 (1-938)

QY 2 GAATTCCTCTTGTGCAAGTCAAAAGAGCCCAACAGAGCGGCGCTCAACCATTCCTCCCA 61
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Db 114 GUAUUAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 62 CAGCAGCC-----AAATCGGGGAGCCCAACATGCTTTTG 100
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 134 SerLeuProLyArgThrLeuGluProLeuAerPthGluYAla1a1aArgSerValLeu 153
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 101 GACCAAGATCCCTCCGCCAGAGCGGCGCCCTGGGAGCGCTCCCTCCCAAAATGCGCT 160
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 154 SerSerPheLeuProProValProSerLeuProThnGluProGluHis----- 170
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 161 TTGCTGGGCGCTTACAGACATGTCAGACGATTCCTCCCTCCGAAACAGCTTGAACC 220
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 171 -----PheProLeuArgYethrValSerGluPro 180
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 221 AACTTGAAGTCCGTTCAAGGCTAAACAGAGAGTGGCTGAGACCGGAGAAAGCACTCCCTC 280
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 181 AsnLeuYbLeuAArgYbLeuProYb--LysSerLeuGluAArgYbArgYbAsnProLeu 199
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 281 CTGCGCTCCCAAGATGGGAGCTGTATTAGCACTTTTAAGAGAAGAGCTGTAGATCACA 340
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 341 GATGCGGAGCGCTGGGCGCTGCTCCGTTGTATAACAGCGACCCGCGCTCCGCGCCCACTT 400
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 218 GluAerSerSerProSerSerSer-----SerThrProAlaSerGluCySerSer 224
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 401 CCCAACAGCTCCCAACAGACCACTCGCTGAGAAAGCTTTACTGGCTCACTCCCAACATC 460
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Db 235 ProAerAerSer-----GluHisGly----- 241
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QY 461 CCCACTAGATGTCCTCCCTACAGACCGGAGCGCTCCCTGTGAGAGCTCCCAACAGATTC 520
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Db 241 ----- 241
QY 521 AGCCTTACAGATCTCTTCTGTGCGCCAAATCTCCCTAGGCTGAGCGCAACGATCACT 580
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 242 -----ProAerProAlaLeuGluSerGluAlaAerGluAer 253
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 561 GTCAACAACTACACACTGACTGCTCCCGAAG----- 613
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 254 --ArgArgThrHisSerThrLeuGluProArgGluProValLeuGluYbAsnProHisAla 272
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 614 ---CTGTGACACAGACAGAGCGGCGGAGGCGCTCCCAATCTCCCTGCGGACAGGTTGC 670
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 273 ProLeuPheLeuHisGluYbLeuGluProGluAla-----GluYbGly 286
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 671 AAGCTTACGCGCAAGTTATGATGACAGACATCTTATCTCTGAGCTGCTGGGCGCTGGCA 730
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 287 ThrLeu----- 288
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QY 731 CTGAGAGCGACAGGAGCGCCCAACGAGGAGATGCTCCCTGCTGAGAGATGCTGTTCCTG 790
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Db      289 -----ProSerArgLeuGlnProIleLeuLeu 298
Qy      791 GAGCAGGCGCCGGGAGCAGAGCACCCTCATGTCGTG-----CCAATC 832
Db      299 AspProSerValSerHisAlaProLeuTrpThrValProGlyLeuGlyProLeuProPhe 318
Qy      833 CACGGCAGTCCCACTAGTACGGGTGAACGTGTGGCCACAGCATGCGGACGTAGGC 892
Db      319 HisPheAlaTrnProLeuLeuThrGlnArgLeuSerGlySer----- 333
Qy      893 AAGCTCCCGGAGCGCCCTGTAGCCGCACTCACTCCTCACCCTGCGCGAGAGTCCC 952
Db      334 -----GlyLeuHisArgProLeuAsnArgThrArgSerGlnProLeuProProSerAla 351
Qy      953 CAGGCGCTGAGCAGCGGTGATGATGCAACAACAGACAGCATTCCTGGAGAAAGCAGAG 1012
Db      352 ThrAlaSerProLeuLeuAlaProLeuGlnProArgGlnAspArgLeu----- 367
Qy      1013 CACGACGAGCTACGATGCGGCAAGATCCTCACCAAGACAGGAGCTGCCAGGAGCCC 1072
Db      368 LysProHisValGlnLeuIleLysProAlaIleSerProProGlnArgProAlaLysPro 387
Qy      1073 ACCACCCACCTTGAAGACAGACAGAGAGAGCTGACGAGACAGACGAGCTTGTGGGG 1132
Db      388 SerGlnLysProArgLeuArgGlnIleProSerAlaGlnAspLeuGlnThr--AspGly 407
Qy      1133 GAGGAGAGCCCTACCATGCCCCGGGAGGAGCTC---CACAGAGTGAGACACACAGAA 1189
Db      407 LysIleValGlyTrpMetAlaAsnAspGlyLeuGlnHisArgGln-----SerIle 424
Qy      1190 GACCTGAGAGACAGACAGACAGAGATGCGGAGAGAGAGAGATTCATCCAGTT 1249
Db      424 ArgLysProProGlnGlyArgGly--SerIleSerLeuGlnGlnHisGlnIleValProPro 443
Qy      1250 AAGACGAGAGAGGCGAGAGCTGTGCTGAGAGAGGCGCCGATTCGAGAGAGCTGTGCT 1309
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Qy      1310 GGAATACAAAATGTTTCTCAGATGCCCAACCGCTGCACCTTTCGACGATGATCAAGCG 1369
Db      459 GlyAspSerValLeu----- 463
Qy      1370 CCCCCTCAGCTGCGCACTGTGCCCCAACAGCCCTGGGCGGTACCCCAATCTCCCTGCT 1429
Db      464 ---IleProLeuAlaGlnValGlyHisArgProLeuSerArgThrGlnSerSerProAla 482
Qy      1430 GCCCTGGGGGGCATGAAGAAACCCCAACCAACCCGCTC----- 1468
Db      483 AlaProValSerMetLeuSerPro-----GlnProThrCysGlnThrGlnValLeuAsn 500
Qy      1469 ---AAGACCTCTTTCACCAACAAGTGTGTCTAGACACGTTCACTGCTAAAGCAACGATGC 1525
Db      501 SerSerGlnThrProAlaTrnGlyLeuValLysTrpAspSerValMetLeuLysHisGlnCys 520
Qy      1526 ATGTGGCGGAACAACACAGTGCACCCCTGACATGCTGGCGGATTCAGACATCTGTGTC 1585
Db      521 SerCysGlyAspAspSerLysHisProGlnHisAlaGlyArgIleGlnSerIleTrpSer 540
Qy      1586 CGGCTGACAGAGACGCGCTGTCTTAGCAGAGTGCAGCGGATCCGAGGTGCCAAAGCCAG 1645
Db      541 ArgLeuGlnGlnLysArgGlyLeuArgSerGlnCysGlyLeuArgGlyArgLysAlaSer 560
Qy      1646 CTGAGTGAAGATTCACACAGTGCACCTGATACCAACACCTGCTATATGGACACAGTCCC 1705
Db      561 LeuGlnGlnLeuGlnSerValHisSerGlnArgHisValLeuLeuValTrpLysAspPro 580
Qy      1706 CTCACACCGCAGAGATAGACACACAGAGATGCTCGTCCATCAGCCGAGAGATGTAT 1765
Db      581 LeuSerArgLeuLysLysLeuAspAsnGlyLysLeuThrGlyLeuLeuAlaGlnArgThrPhe 600
Qy      1766 GCTGTGCTGCTTTGTGTGGGGCATCGGGGTGACAGTACACCGTGTGAATGAGATGCAC 1825

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Db      601 ValMetLeuProCysGlyGlyValGlyValAspThrAspThrIleTrpAsnGlnLeuHis 620
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Db      621 SerSerAsnAlaAlaArgTrpAlaAlaGlySerValThrAspLeuAlaLeuValAla 640
Qy      1886 GCAGAGAGCTCAAGAAATGATTTGGCATATCCGCGCCCAAGACACACCGCGAGAA 1945
Db      641 SerArgGlnLeuLysAsnGlyPheAlaValAlaArgProProGlyHisHisAlaAspHis 660
Qy      1946 TCCACAGCCATGAGATTTCTTTCATCTGTATGCCATCACCCCAAAATCTCTACAG 2005
Db      661 SerThrAlaMetClyPheCysPhePheAsnSerValAlaIleAlaCysArgGlnLeuGln 680
Qy      2006 CAGAAGTTGAACGTGGGACAGGCTCATCGTGAACCTGAGACATTCACCATGGCAATGCG 2065
Db      681 GlnHisGlyLysAlaSerLysIleLeuIleValAspTrpAspValHisHisGlyAsnGly 700
Qy      2066 ACCCAGACGCGCTTTCACATGACCCCTGTGTCTGTACATCTCTGTGATCGTATGAC 2125
Db      701 ThrGlnGlnThrPheTrpGlnAspProSerValLeuTrpIleSerLeuHisArgHisAsp 720
Qy      2126 AACGGGAATCTTCTTTCAGAGCTTGTGGGCTCCCTGAAAGAGTGTGTGAGAGACAGCCG 2185
Db      721 AspGlyAsnPhePheProGlySerGlyAlaValAspGlnValGlyThrAlaSerGlyLys 740
Qy      2186 GGGTACATGTGAACGTGGCATGACAGAGAGGTGTGACCCCCCAATGAGACGTGAG 2245
Db      741 GlyPheAsnValAsnValAlaTrpAlaGlyLysLeuAspProPheMetClyAspProGln 760
Qy      2246 TACCTTACAGCCTTCACAGACAGTGTGATGCCATTTGCCACGAGTTCTCACCTGATGTC 2305
Db      761 TyrLeuAlaAlaPheArgIleValValMetProIleAlaArgGlnPheAlaProAspLeu 780
Qy      2306 GTCTTGTCTCGCGCGGTTTGTATGCTGTGTAAGACATCTGTCTCTGTGGTGTGCTAC 2365
Db      781 ValLeuValSerAlaGlyPheAspAlaAlaGlnGlyHisProAlaProLeuGlnGlyLys 800
Qy      2366 TCTGTACCGCCAGATGTTTGGCCACTTGACACAGGAGCTGATGACCCCTGGCAGGAGGC 2425
Db      801 HisValSerAlaLysCysPheGlyTyrMetTrnGlnGlnMetLysLeuAlaGlyGly 820
Qy      2426 CCGGTGTGTGCGCCCTGAGAGGAGGCGCATGACTTGACCCGCACTGTGATGCTTGA 2485
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Qy      2486 GCTTGTGTCTCGGCTTGTCTCACTGTAAAGCTGACAGCCCTTGATAGAGCAGCTTTCAG 2545
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Qy      2546 CAATAACCCCAACATCAACGACAGGCGCATGAGAAAGTCAATCGAGATCCAGACCA 2605
Db      861 GlnLysProAsnMetSerAlaIleArgSerLeuGlnAlaValAlaArgValHisAspGly 880
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Qy      2767 CCGGACAGAGAGCCCATGAGCAGAGAG 2793
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RESULT 7  
 US-09-644-827B-8  
 ; Sequence 8, Application US/09644827B

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; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caspase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644,827B
; PRIORITY FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-644-827B-8

Alignment Scores:
Pred. No.: 1,07e-108 Length: 1200
Score: 1739.50 Matches: 423
Percent Similarity: 50.75% Conservative: 121
Best Local Similarity: 39.46% Mismatches: 239
Query Match: 32.54% Gaps: 289
DB: 4 Gaps: 26

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DB 174 GlnuRgThrValHisProAsnSerProGlyTLeProTyrArgSerGlnGlyProCysSer 193
QY 78 GGGGAGGCCCAACATGCTTTGAGCAGAGTTCCCTCCACAGAGCGGCCCTTGGA 137
DB 194 GlyGln-CysProCys-----SerValProThrProLeuylGlnProTyrPht 209
QY 138 CGCC-----TC 143
DB 209 sSerPheCysArgThrLeuGlnProLeuGlnThrGlnGlyAlaThrArgSerMetLeuSe 229
QY 144 CCGCTTCAACAAGCGCTTTCCTGCTGGG---CCCTTACAGACGTCAGAGACTTCCCTTCC 200
DB 229 r-SerPheLeuProProValProSerLeuProSerAapProProGlnHisPheProLeuA 249
QY 201 GCAAAACAGCGCTGTGAACCACTTGAAGAGTGCCTTCAAGGCTTAAACAGAGGTGGCTG 260
DB 249 rGlySerThrValSerGlnProAsnLeuylSerArgTyrLysProLys---LysSerLeuG 268
QY 261 AGCGAGAGACAGTCCCTCTCGCTGCGCAAGATGGAGACTTTATTGACACTTTAAGA 320
DB 268 lValrGArgLysAsnProLeuLeuArgLysGlnSerAlaPro-----ProSerLeuArgA 286
QY 321 AGAGAGCTGTGAGTACACAGTGCCTGGGCTGGGCGCTGCTGCTGTGAACAGCGCAC 380
DB 286 rGArgProAlaGlnThrLeuGlnLysAspSerSerProSerSerSer-----SerThrP 303
QY 381 CCGGCTCCCGGCGCCAGCTTCCCAACAGCTCCCAACAGACACACATGCTGAGAAATGGCTTTA 440
DB 303 rAlaSerGlyCysSerSerProAsnAspSerGlnHis----- 315
QY 441 CTGGCTCAGTCCCAACATCCCACTGAGATGCTCCTTCAAGACCGAGCCCTCTCTGG 500
DB 316 --GlyProAsnProGlnLeuGlnSerGlnAlaLeuGlnGlnArgLeuArgLeuGln 335
QY 501 ACAGCTCCCAACCAAGTCAAGCTTCAACAGTCTCTCTCTGCGCAACATGCTCCCTAG 560
DB 335 lValrSerValAlaProPheAlaLeuProThrValSerLeuLeuProAlaAlaLeuThrLeuG 355
QY 561 GGCTGACGAGCCACGCTCATGTGTCAACAATCAACACTCACTGCTCCCGCAAGCTGTGCA 620
DB 561 lValrSerValAlaProPheAlaLeuProThrValSerLeuLeuProAlaAlaLeuThrLeuG 355

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DB 355 lLeuProAla-----ProA 360
QY 621 CACAGCAGAGGCGCAGAGGCGAGCCCTCCAGTCCCTGCGGCAAGGTCAGCGTACCG 680
DB 360 lAaRgAlaAspSerAapArgArgThrHisProThrLeuGlnProAlaGlyProLeuLeuG 380
QY 681 GCAAGTTCATGACACATCTCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740
DB 380 lYserProHisThrProLeuPheLeuProHis-----GlyLeuGlnProGlnAlaG 397
QY 741 ACAGGAGCCCCACAGGAGATGCTCTCTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
DB 397 lGlyThr-----LeuProSerArgLeuGlnProLeuLeuLeuAspProSerG 414
QY 801 GGCAGCAGACACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 860
DB 414 lYserHisAlaProLeuLeuThrValProGlyLeuGlyProLeuProPheHisPheAlaG 434
QY 861 AACGTGCGCCACAGCATCGGACGAGTGAAGAGTCCCGCGCATCGGCTGAGCC 920
DB 434 lSerLeuMetThrThrGlnArgLeuSerGlySer---GlyLeuHisThrProLeuSerA 453
QY 921 GCACTCAGTCTTACCGCTGCGCAAGATCCCAAGCC----- 958
DB 453 rGThrArgSerGlnProLeuProProSerAlaThrAlaProProProGlyProMetG 473
QY 959 -----CTGCAGCAGCTGTGATGCAACAACAGCAGCAGCTTCTGGAAGAGCA 1010
DB 473 lndProArgLeuGlnGlnLeu-----LysThrHisValGlnValLLeuArgSer- 489
QY 1011 AGCAGCAGCAGTACAGCTGGGCAAGATCTTCAACCAAGAGGAGCTCCAGGAGC 1070
DB 490 -----AlaLysProSerGlnLysProArg----- 497
QY 1071 CCAACACCACTGAGAGACAGAGAGAGCTGACGAGCAGAGAGCTTCTGCTG 1130
DB 497 ----- 497
QY 1131 GGGAGGAGCGCTGACCATGCCCCGGAGGCGTCCACAGAGATGAGACACAGGAAG 1190
DB 498 -----LeuArgGlnI 501
QY 1191 ACCTGAGAGAGAGAGAGAGAGATGGGAGAGAGAGAGATTCATCAGAGTTA 1250
DB 501 lProSerAlaGlnAspLeuGlnThrAspLys----- 511
QY 1251 AGGACGAGAGGCGAGAGTGT-----GCTGAGAGAGGCGCGACTTGAGAGGCTTG 1304
DB 512 -----GlyGlyProGlnGlnValAlaAspArgGlyLeuGlnHisArgGlnLeuG 528
QY 1305 GTGCTGATTCAAAAAAGTCTTCTCAAGTCCCAACCGCTGCAACTTTGCAAGTGTACC 1364
DB 528 lYHisGlyGln-----ProGlnAlaArgLysProAlaProLeuGln-----G 542
QY 1365 AACGCGCC----- 1372
DB 542 lHisProGlnValLeuLeuThrGlnGlnAlaArgLeuAlaGlyArgLeuProArgGlys 562
QY 1373 -----CTCAGCTTGGCCACTGTGCCCAACCAAGCTTGGCGCTGA 1412
DB 562 rThrGlnAspThrValLeuLeuProLeuAlaGlnGlnGlyHisArgProLeuSerArgA 582
QY 1413 CCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1453
DB 582 lAclnSerSerProAlaAlaProAlaSerLeuSerAlaProGlnProAlaSerGlnAlaA 602
QY 1454 -----CCAGACCAACCGTCAAGACACTC---TTCACACAAAGTGTGCTG 1496
DB 602 rGValLeuSerSerSerGlnThrProAlaArgThrLeuProPheThrThrGlnLeuIleT 622
QY 1497 ACAGCAGCTTCATGTAAAGACACAGTGTGCGGGAACACACACAGTGCACCTGTAGC 1556
DB 622 lYAspSerValMetLeuLysGlnCysSerCysGlyLysAspSerAArgHisArgProGlnHis 642

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QY 1557 ATGCTGGCCGGATCCAGAGCATCTGTGCTCCGGCTGCAGAGACAGCGCTTGACCAAGT 1616
Db 642 isalaglYargilleginsertiletrpserArgleuGlnGlyArgGlyLeuArgSerGlnC 662
QY 1617 GCGAGCGCAATCCGAGGTCGGAAGCCACGCTAGATGATCCAGACAGCTGACATCTGCAAT 1676
Db 662 ysGlnCysLeuArgGlyArgLysAlaSerLeuGlnGlnLeuGlnSerValHisSerGlnA 682
QY 1677 ACCACACCTGCTCTATGGACACGATCCCTCAACCGGACAGACTAGACAGCAAGAGT 1736
Db 682 rghisValLeuLeuTyrgLysThrAsnProLeuSerArgLeuLysLeuAspAsnGlyLysL 702
QY 1737 TGTCTGCTTCATCAGCCAGCAAGATGTATGCTGTGCTGCTGTGCTGTGCTGTGCTGCTG 1792
Db 702 euaIagIyleuLeuIagIlnArgMetCpheValMetLeuProCysGlyGlyValGlyProl 722
QY 1792 ----- 1792
Db 722 euaIaThrLysSerAlaPheLeuAlaSerLeuAlaProThrValProGlnGlyLeuSerA 742
QY 1792 ----- 1792
Db 742 rglValSerTrpGlyLeuLysProProGlyProAsnProLysSerArgProAlaProC 762
QY 1792 ----- 1792
Db 762 ysrProTrpGlyProGlyArgGlyValGlyLysThrThrProLeuGlyProGlySerCysValL 782
QY 1793 ----- 1793
Db 782 ysrProTrpMetMetArgAlaLeuThrLeuAlaProGlnValAspThrAlaSerThrLysTrpA 802
QY 1815 ATGAGATGACACTGCTCCAGTGTGTGTCGTCATGGACAGTGGAGCTGCTGACAGCTGGCCT 1874
Db 802 snGlnLeuHisSerSerSerAsnAlaAlaArgTrpAlaAlaGlySerValThrAspLeuAlaP 822
QY 1875 TCAAGGTGCTGTCAGAGAGACTCAAGATGATGATTTGTCATCATCCGCGCCCGCCAGACACC 1934
Db 822 heIysValAlaSerArgGlnLeuLysAsnGlyPheAlaValAlaArgProProGlyYHisH 842
QY 1935 ACCGCGAGGAGATCCAGAGCATGCTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1994
Db 842 isAlaAspHisSerSerThrAlaMetGlyPheCysPhePheAsnSerValAlaIleAlaCysA 862
QY 1995 AACTCTACAGACAGAGTGAACGTGAGCAAGGCTCATGTCATGTCGATGTCGATGTCACCC 2054
Db 862 rglGlnLeuGlnGlnGlnSerLysAlaSerLysIleLeuIleValAspTrpAspValHisH 882
QY 2055 ATGGCAATGGCAATCCAGACAGCGCTTCTACAAATGACCCCTGTGCTGTACATCTCTGTC 2114
Db 882 isGlyAsnGlyThrGlnGlnThrPheTyrgLysProSerValLeuTyrgLysSerLeuH 902
QY 2115 ATGGCTATGCAATGGGAATCTTCTTCCAGGCTCTGCGGCTCCCGAAGAGATTGTGTGAG 2174
Db 902 isArgHisAspAspArgLysAsnPhePheProGlySerGlyAlaValAspGlnValGlyAlaG 922
QY 2175 GACACAGCGTGGGGTACAAATGTGAACGTGTCATGACAGAGAGTGTGACCCCGCCCATTTG 2234
Db 922 lysGergLysGlnGlyPheAsnValAsnValAlaAlaTrpAlaGlyGlyLeuAspProPrometG 942
QY 2235 GAGACGTGAGTACTTTACAGCCTTCCAGACAGTGTGATGCCCATTTGCCACGAGTTCT 2294
Db 942 lysPsrProGlnTyrgLysAlaAlaPheArgLysValValMetProIleAlaArgGlnPheS 962
QY 2295 CACCTGATGTGCTCTAGTCTCCGCGGCTTGTATGCTGTGTGAAGACATCTGCTCTCTC 2354
Db 962 erProAspLeuValLeuValSerAlaGlyPheAspAlaAlaGlnGlyHisIlePheAlaProL 982
QY 2355 TGGGTGCTACTGTGTCACCGCCAGATGTTTGGCAGCTTGCACGACGAGCTGATGACCC 2414
Db 982 euGlnGlyTyrgHisValSerAlaLysCysPheGlyTyrgMetThrGlnGlnLeuMetAsnL 1002

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QY 2415 TGGCAGGGGGCCGGGTGCTGCTGCGCTTGGAGAGGCCCATGACTTGAACCGCATCTGTG 2474
Db 1002 euaIagIyGlyValaValAlaLeuAlaLeuGlnGlyGlyHisAspLeuThrAlaIleCysA 1022
QY 2475 ATGCCCTGATGCTGTGTCTGCGGCTCTGCTCAGTGTAAAGCTGACGACCTTGATGAG 2534
Db 1022 sPlAspSerGlnAlaCysValAlaAlaLeuLeuGlyLysAsnArgValaAspProLeuSerGlnG 1042
QY 2535 CAGTCTTGCAGCAAAAAGCCCAATCAACGACAGTGGCCACGCTAGAGAAATCATGACGA 2594
Db 1042 lncLysTyrgLysGlnLysProAsnLeuAsnAlaIleArgSerLeuGlnAlaValIleArgV 1062
QY 2595 TCCAGAGCAAAACACTGAGACTGTGTGCAGAAAGTTCGCCCTGTGCTGGCCGCTCCCTGC 2654
Db 1062 AlHisSerLys----- 1065
QY 2655 GAGGGGCCAAGCAGGTGACCGCAAGACCGCAATGTGAACGCCATGAGCTTGCTGT 2714
Db 1066 -----CysGlyAspGlyThrLeuAlaGlnLeu----- 1074
QY 2715 GGTGGGGGCCGAACAGGCCCAAGCTGCGGACCGCGGAACACAGCCCGGACG 2774
Db 1075 -----ArgLeuLysAspLeuGlyGlyThrLeuProHisArgGlyG 1088
QY 2775 GGAAGCCCATGAGACAGAGAGCTGCCCTGTGAC 2806
Db 1088 lnlLeuGlnLysPheArgCysGlnProGlyAsp 1098

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## RESULT 8

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US-09-644-827B-7
; Sequence 7, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caspase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644, 827B
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-644-827B-7

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## Alignment Scores:

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Pred. No.: 1,12e-108 Length: 1428
Score: 1739.50 Matches: 423
Percent Similarity: 50.75% Conservative: 121
Best Local Similarity: 39.46% Mismatches: 239
Query Match: 32.54% Indels: 289
DB: 4 Gaps: 26

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US-09-502-945-2 (1-2885) x US-09-644-827B-7 (1-1428)

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QY 21 CAAAGAGCCCAACAGGCGGCTTCAACCATTCCTCCACAGACAC---CCAAATGCT 77
Db 400 GluArgThrValHisProAsnSerProGlyLysProTyArgSerGlnGlyProCysSer 419
QY 78 GGGAGCCCAACATGCTTCTTTGACCAAGATTCCTCCCGACAGCGGCGCCCTTGGGA 137
Db 420 GlyGln-CysProCys-----SerValProThrProLeuLysGlnProTrpH 435
QY 138 CGCG-----TC 143
Db 435 sSerPheCysArgThrLeuGlnProLeuGlnLysGlnAlaThrArgSerMetLeuSe 455

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Qy	144	CTCTCTAACAATGCTCTTGGCTGGG-----CCTTAGACAGTGCAGACAACTCTCCCTCC	200
Db	455	r-SetPrbLeuProProValProSerLeuProSerAspProProGlnIvPrbPrbLeuA	475
Qy	201	GCAAAACAGCCTCTTAACCAACTTGAAGATGCGCTTCAAGGCTAAACAGAAAGTGCGTG	260
Db	475	rglygthValSerGluProLeuGlnLeuVbLeuAgyTyrlLeuProlys--LysSerLeuG	494
Qy	261	AGCGGAGAGACGTCCTCCCTCGCTGCGCAAGATGGAGCTGTATATTAAGCACTTTAAGA	320
Db	494	lurAgygTygAaAnPrbLeuLeuAgyVgVluseValAPro-----ProSerLeuAgyA	512
Qy	321	AGAGAGCTGTGAATCATCAGGTGCCGGGCGCTGGGGCGCTGCTCGCTGTATACAGCGGAC	380
Db	512	rgATgPrbAlAgIvthrLeuGlyAAspSerSerProSerSerSer-----SerThrP	529
Qy	381	CCGGTCTGGGGCCGAGCTCTCCCAACACTCCCAAGACACATGCTAGAAATGGCTTTA	440
Db	529	roAlAspGlyCyAspSerProAaAnAspSerGlnHis-----	541
Qy	441	CTGGCTCAGTCCGCGCAATCCCACTGAGATGCTCTCTCAGACACCGACCCCTCTCTGG	500
Db	542	--GlyProAnPrbProLeuGlnLysGrluVAlaLeuGlnGlyGlnArgLeuArgLeuGlnG	561
Qy	501	ACAGCTCCGCGCAACGATTCAAGCTTTCAAGCTCTCTCTCTCTGCGCAACATCTCCCTAG	560
Db	561	lurThrSerValAlAProPhbAlaLeuProThrValSerLeuLeuProAlaIleThrLeuG	581
Qy	561	GGCTGCAGGCGGACGGTCACTGTGCACCACTCAACCTCACTGCTCCCGCGAAGCTGTGA	620
Db	581	lLeuPrbAla-----	620
Qy	621	CACAGCAGAGAGGCGAGAGGCGCTTCAAGTCTCGGACGAGGATGGACAGCTGACCG	680
Db	586	lAaVgVAlAAspSerAspArgArgThrGlnIvProThrLeuGlnIvProArgGlyProIleLeuG	606
Qy	681	GCAAGTTCAATAGACACATCTCTATCTCTGAGCTGCTGAGCGCTGAGCACTGAGAGGCG	740
Db	606	lYserProHlVbThrProLeuPrbLeuProHlA-----GlyLeuGluProGlnAlaG	623
Qy	741	ACGGGAGGCGCGGAGGATGCTCTCTGCTGCGACATGTGTCTGTCTGAGACAGGCGCC	800
Db	623	lYgIvThr-----LeuProSerAArgLeuGlnProIleLeuLeuLeuAspProSerG	640
Qy	801	GGCAGCAGACACGCTCATGCTGCTGCGACATCCACGGGCAAGTCCCACTAGACAGGCTG	860
Db	640	lYserHlAlAProLeuLeuThrValProGlyLeuGlnIvProLeuProHbHlVbAlaG	660
Qy	861	AACGTGTGCGCAGCAGATCGCGAGCGATGAGCAAGCTCCCGGCAATCGGCGCTGAGCC	920
Db	660	lInserLeuMetThrThrGluArgLeuSerGlySer--GlyLeuHlVbPrbProLeuSerA	679
Qy	921	GCACTCAGTCTCAACGCTGCGCGCAGAGTCCCAAGGCG-----	958
Db	679	rgThrArgSerGluProLeuProProSerAlaIvPrbAlaProProProGlyProMetG	699
Qy	959	-----CTGCAGAGCTGTGCATGCACAACAAGCAGACACAGTCTCTGAGAAAGCAGA	1010
Db	699	lInProArgLeuGlnGlnIvLeu-----LysThrHlSValGlnAlaIleLysArgSer	715
Qy	1011	AGCAGCAGACACTACAGCTGGGCAAGATCTCACCAACAGAGGGAGCTGCGCAGGAGCG	1070
Db	716	-----AlaLysProSerGluLysPrbArg-----	723
Qy	1071	CCACCAACCCCTGAGGAGACAGAGAGAGCTGACGAGACAGACAGAGGTCTTGTCTGG	1130
Db	723	-----	723
Qy	1131	GGGAGGAGCCCTGACCACTGCCCGGGAGGGGCTCCACAGAGATGAGACACAGAGAG	1190
Db	724	-----LeuArgGlnIv-----	727

[illegible]

Db 1068 isAlaAspHisSerThrAlaMetGlyPheCysrPhePheAsnSerValAlaIleAlaCysA : 1088

1995 AACTCTACACAGCAAGATTGAACGTGGGCAAGCTTCATCGTGAATGGAGACATTAC 2054

Db 1088 rGlnIleuGlnGlnGlnSerLysAlaSerLysIleLeuIleValAspTrpAspValHis 1108

Qy 2055 ATGGCAATGGCAACCCAGAGGCGTTTTCATATGACCCCTCTGTCTCAATCTCTGCG 2114

Db 1108 isGlyAsnGlyThrGlnGlnInhrPheTyrGlnAspProSerValLeuIlyrIleSerLeuH 1128

Qy 2115 ATCGCTATGACAAACGGGAATCTCTTCCAGGCTCTGGGGCTCTCGAAGAGTTGGTGAG 2174

Db 1128 isAlaGHisAspAspGlyAsnPhePheProGlySerGlyAlaValAspGluValGlyAlaG 1148

Qy 2175 GACCAAGCGGTGAGGTCAATGTGAACGTGGACATGACAGAGGTGTGGACCCCGCATTTG 2234

Db 1148 lySerGlyGlyuGlyPheAsnValAsnValAlaTrpAlaGlyGlyLeuAspProMetG 1168

Qy 2235 GAGACGTGGAGTACCTTTCACGCTTCAGACACAGATGTATGCCCCATTCGCAAGTTCT 2294

Db 1168 lyAspProGlyIlyrLeuAlaIleAspAspGlyIleValValMetProIleAlaTrpGlyPhe 1188

Qy 2295 CACCTGATGTGCTCTAGTCTCCGCGGGGTTTGAATGTGTGAAGACATGTCTCTCTC 2354

Db 1188 erProAspLeuValIleuValSerAlaGlyPheAspAlaIleGlyIlyrProAlaProL 1208

Qy 2355 TGGGTGCTACTTGTGTCAACCGCAAGATTTTGGCACTTGAACGAGGAGTGTAGACC 2414

Db 1208 euGlyGlyIlyrHisIleValSerAlaLysCysrPheGlyIlyrMetThrGlnIleuMetAsnL 1228

Qy 2415 TGGCAGGGGGGCCGGGTGTCTGTGCTTCAGAGGAGGCGCATGATTTGACCGGCATCTGTG 2474

Db 1228 euAlaGlyGlyAlaValAlaIleuAlaLeuGlyGlyGlyIlyrAspLeuThrAlaIleCysA 1248

Qy 2475 ATGCTCTGAAGCTTGTGTCTCGGTCTGTGCTCAAGTGAAGTGAAGCTTGAGCGCTTGATGACG 2534

Db 1248 spAlaSerGlnAlaCysValAlaAlaIleuLeuGlyAsnAspValAspProLeuSerGlyG 1268

Qy 2535 CAGTCTTGACACAAAGCCCAACATCAACAGGAGTGGCCCACTTGAAGAAATCTCATCGA 2594

Db 1268 IuGlyTrpLysGlnIlyrProAsnIleuAsnAlaIleArgSerLeuGlnAlaValIleArgV 1288

Qy 2595 TTCAGAGCAACATGTGAGCTGTGTGCAAGATTGCGCGTGTGTGGCCGGTCCCTGCG 2654

Db 1288 alHisSerLys----- 1291

Qy 2655 GAGGGGCCCAAGCAGTGTAGACCCAGAAAGCCGAAATGTGAACCGCATAGGCTTGCTGT 2714

Db 1292 -----CysGlyAspGlyThrIleuAlaGlnLeu----- 1300

Qy 2715 GGTGGGGCGCAACAGGCCCAAGCTGGGGCAGCCCGGGAGACAGACCCCGAGCGGAGCA 2774

Db 1301 -----ArgLeuLysAspLeuGlyGlyThrLeuProHisArgGlyG 1314

Qy 2775 GAGGCCATGAGCAGCAGAGCTGCGCTTGTAC 2806

Db 1314 InIleuGlyPheArgCysGlnProGlyAsp 1324

RESULT 9

US-09-644-827B-6

/ Sequence 6, Application US/09644827B

/ Patent No. 6762283

/ GENERAL INFORMATION:

/ APPLICANT: WALLACH, David

/ APPLICANT: SCHUCHMANN, Marcus

/ APPLICANT: GONCHAROV, Tanya

/ TITLE OF INVENTION: Caspase-8 Interacting Proteins

/ FILE REFERENCE: WALLACH-26

/ CURRENT APPLICATION NUMBER: US/09/644,827B

/ CURRENT FILING DATE: 2000-08-24

/ PRIOR APPLICATION NUMBER: 132105

/ PRIOR FILING DATE: 1999-09-28

/

[illegible]

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Db      270 LeuAlaPheValAlaSerArgGluLeuValSerGlnPheAlaValAlaArgProPro 289
Qy      1928 GGAACACACCCGAGGAAATCCACAGCCATGGGATTCCTTCAACTCTGTGACATC 1997
Db      290 GlyHisHisAlaSerHisSerThrAlaMetCysPhePheAsnSerValAlaIle 309
Qy      1988 ACCGAAACCTCTACAGAGAAAGTTGAACGTGGGACAGGCTCATCGTGAATGGGAC 2047
Db      310 AlaCysArgGlnLeuGlnGlnSerLysAlaSerLysIleLeuIleValAspTTPAsp 329
Qy      2048 ATTCAACCATGGCAATGGCACCCAGCCGCTTTCATATGACCCCTGTGCTTACATC 2107
Db      330 ValHisHisGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 349
Qy      2108 TCTCTGATGCTATGACAAAGGAACTTCTTTCAGGCTCTGGGGCTCTCGAAGAGTT 2167
Db      350 SerLeuHisArgHisAspAspGlyAsnPheProGlySerGlyAlaValAspGluVal 369
Qy      2168 GGTGAGGACACAGGCGTGGGATACATGTGAACGTGGACATGACAGAGGTGTGACCCC 2227
Db      370 GlyAlaGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 389
Qy      2228 CCCATTGAGACGTGATACCTTACAGCCTTACAGACAGTGTGATGCCATTGCCAC 2287
Db      390 ProMetCysAspProGluGlyTrpLeuAlaAlaPheArgIleValValMetProIleAlaArg 409
Qy      2288 GATTTCTACACTATGATGTGCTTCTGCTCCGCGGCTTGTGATGCTGTAAGACATCTG 2347
Db      410 GluPheSerProAspLeuValIleValSerAlaGlyPheAspAlaAlaGluGlyHisPro 429
Qy      2348 TCTCTGTGGGTGACTACTGTGACCCGACAGATGTTTGGCCATGACAGGACAGCTG 2407
Db      430 AlaProLeuGlyGlyTrpHisValSerAlaLysCysPheGlyTrpMetThrGlnGlnLeu 449
Qy      2408 ATGACCTTGCAGAGGCGCGGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2467
Db      450 MetAsnLeuAlaGlyGlyAlaValIleValLeuAlaLeuGlyGlyHisAspLeuThrAla 469
Qy      2468 ATCTGTGATCCTCTGAAAGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2527
Db      470 IleCysAspAlaSerGluAlaCysValAlaAlaLeuLeuGlyAsnArgValAspProLeu 489
Qy      2528 GATGAGGACATCTTGCAGAAAGCCCAACATCAAGCAGTGGCGCTGTGCTGCTGCTG 2587
Db      490 SerGlnGlnGlyTrpLysGlnLysProAsnLeuAsnSerIleArgSerLeuGluAlaVal 509
Qy      2588 ATCGAGATCCAGAAACATGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2647
Db      510 IleArgValHisSerLysTrpGlyCysMetGlnArgLeuAlaSerCysProAspSer 529
Qy      2648 TCCCTGCGAGGCGCCAGACAGTGTGACCGAAGACCCGAAT-GTGAAGCCCATGCGC 2706
Db      530 TrpValProArgValProGlyAlaAspLysGlnGluValAlaValIleThrAlaLeuAla 549
Qy      2707 TTCTGTGTGTGGGG-----GCCGAACAGGCCCAAGCTCGGAGCGCGGAACAGC 2760
Db      550 SerLeuSerValGlyIleLeuAlaGluAsp----- 559
Qy      2761 CCCAGCGGACAGAGAGCCCATGAGACAGAG 2793
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CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPacSeqFormatter Version 0.9
SEQ ID NO 649
LENGTH: 706
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)---(0)
OTHER INFORMATION: Polypeptide Accession Number YNL021W
US-09-538-092-649

Alignment Scores:
Pred. No.: 4,56e-37 Length: 706
Score: 672.00 Matches: 162
Percent Similarity: 50.40% Conservative: 87
Best Local Similarity: 32.79% Mismatches: 165
Query Match: 12.57% Indels: 80
DB: Gaps: 15

US-09-502-945-2 (1-2885) x US-09-538-092-649 (1-706)

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Db      2 AspSerValMetValLysLysGluVal-----Leu 11
Qy      1295 GAGAGGCTGTGCTGTGATGACAAATACTGTCTCAGATGCCACCGCTGACACTTTG 1354
Db      12 GluAsnProAspHisAspLeuLysArgLysLeuGlnGlnLys----- 26
Qy      1355 CAGGTATCCAGAGCGCCCTCAGCTGCGCACTGTGCCACCAAGCCTGCGCGTACC 1414
Db      27 -----GluGlnGlnAsnSerLeuSerThr-----SerLysSer 38
Qy      1415 CAATCTCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
Db      39 LysArgGlnValIleValProValCysMetProLysIleHisSerProLeuLys--- 57
Qy      1475 CTCTTACCAACAGTGTGTGCTGACAGCTGATGCTTAAGACCAAGTGCATGTGCGG 1534
Db      58 -----ThrIleLysCysTrpAspValArgMetArgTrpHisAlaLysIlePheThr 74
Qy      1535 AAC-----ACACAGTGCACCTGACATGCTGCGCGATGCCAGACCTGCG 1582
Db      75 SerTrpPheGluTrpIleAspProHisProGluAspProArgArgIleTrpArgIleTrp 94
Qy      1583 TCCCGCTGACAGACAGAGCTGCTTACGAG----- 1615
Db      95 LysIleLeuLeuAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 114
Qy      1616 -----TGCAGAGGATCCGAGGTGCAAGACGACGCTGATGATGATGATGATGATGATG 1666
Db      115 GlyAspLeuMetLeuLysIleProValArgAlaAlaThrSerGlnGlnIleLeuGluVal 134
Qy      1667 CACTGAAATACACAC---ACCTGCTCTATGGACAGTCCCTCAACCGGACGAAGTA 1723
Db      135 HisThrLysGlnHisLeuGlnPheIleGlnSerThrGlnLysMetSerArgGlnGlnLeu 154
Qy      1724 -----GACAGCAAGAAAGTTGCTCGGTCCTCATGACCAAGATGATGCTGTGCTGCT 1777
Db      155 LeuLysGlnThrLys----- 160
Qy      1778 TGTGGGGGATCGGGGTGACAGTGCACAGGTGGAATGAGATGCACTCTCCAGAGCT 1837
Db      161 -----GlyAspSerValTrpPheAsnAspSerTrpAlaSer 173
Qy      1838 GTGCGATGACAGTGGCTGCTGCTGAGAGTGGCTTCAAGTGTGCTGACAGAGCTG 1897

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Db      174 AlaArgLeuProCysGlyGlyAlaIleGluAlaCysLeuValAlaValGluGlyArgVal 193
QY      1898 AAGAATGATGATTCGCATCATCCGACCCCGACAGACACACCGGAGGAATCCAGCCATG 1957
Db      194 LysAsnSerLeuAlaValAlaGProProGlyHnHisValGluProGlnAlaAlaGly 213
QY      1958 GGATTCCTGCTTTCTTCAACTCTGTAGCCCATCCGCAAAA-----CTCTTACAGCCAGAG 2011
Db      214 GlyPheCysLeuIlePheSerAlaValAlaAlaAlaValAsnIleLeuIleuValAsnTyrPro 213
QY      2012 TTGAAGTGGGCAAGGCTTCATCGTGAAGTGGAGCATTCACATGGGCAATGGCACCCAG 2071
Db      234 GluSerValArgArgIleMetIleLeuAerTyrAspIleHisValGlyAsnGlyTyrGln 253
QY      2072 CAGGCGTTCTACATGACACCCCTGCTGCTTACATCTCTGTGATCGCTATGACAAAGG 2131
Db      254 LysSerPheTyrGlnMetArgGlnValLeuTyrValSerIleuHisArgPheGluMetGly 273
QY      2132 AACTCTTTCCAGGCTCT-----GGGCTCTCGAGAGAGTTGGTGGAGGACAGGCTG 2185
Db      274 LysTyrTyrProGlyTyrIleGlnGlyGlnTyrAspIleHisValGlyGlyGlyGly 293
QY      2186 GGATTAACATGTGAACGCGGATG---ACAGAGCTGTGACACCCCGCATTTGAGACGTG 2242
Db      294 GlyPheAsnCysAsnIleHisTyrProValGlyGlyVal-----GlyAspAla 309
QY      2243 GAGTACCTTACACCTTCAGAGACATGTGATGATGATGATGATGATGATGATGATGATGAT 2302
Db      310 GluTyrMetTyrLysPheGluGlnValValMetProMetGlyArgGluPheIleProAsp 329
QY      2303 GTGGCTCTAGCTCTCCGCGGGTTGATGCTGTGAAAGACATGTCTCTCTGGGGTGC 2362
Db      330 LeuValIleIleSerSerGlyPheAspAlaAlaAspIly-----AspThrIleGlyGln 347
QY      2363 TACTGTGTACCGGACAGATGTTTGGCACTTGAACGAGGACATGATGACATGATGACATG 2422
Db      348 CysHisValThrProSerCysTyrGlyGlnMetThrHisMetLeuIleuValAsnArg 367
QY      2423 GGCGGGGTGGTGCATGGCCCTGAGAGGAGGACATGATGATGATGATGATGATGATGATGAT 2482
Db      368 GlyAsnLeuCysValValLeuGluGlyGlyTyrAsnLeuAspAlaIleAlaAsnSerAla 387
QY      2483 GAAGCTTGTGTCTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2542
Db      388 LeuSerValAlaValValIleGlyGluProProAspGluLeuProAspProLeuSer 407
QY      2543 CACCAAAAGCCCAACATCAACGACGAGTGGCCACCGTGAAGAAATGATCCAGATCCAGAG 2602
Db      408 AspProLysProGlyVal-----IleGluMetIleAspIleValIleArgLeuGlnSer 425
QY      2603 AAACACTGAGCTGTGTGAGAAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2644
Db      426 LysTyrTyrAsnCysIlePheArgLysArgHisAlaAsnSerGly 439

RESULT 11
US-09-270-767-45990
; Sequence 45990, Application: US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homologer et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1999-33-17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45990
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-45990
```

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Alignment Scores:
Pred. No.: 9,47e-30 Length: 527
Score: 562.50 Matches: 134
Percent Similarity: 50.63% Conservative: 67
Best Local Similarity: 33.75% Mismatches: 139
Query Match: 10.52% Indels: 57
DB: 4 Gaps: 13

US-09-502-945-2 (1-2885) x US-09-270-767-45990 (1-527)
QY      1484 ACAAGTGTGTCTACAGACATTCATGCTAAAGCAACCAATGATGTCGGGAAACACAC 1543
Db      54 ThrAlaLeuIleTyrAspIleuSerMetSerGlnHisCysCysLeuTyrAspIleuHis 73
QY      1544 GTGCAC---CTGAGCATCTGACCGGATCCAGAGCATCTGGCTCCGGCTGACAGAGACA 1600
Db      74 TyrGluCysProGlu-----ArgPheThrArgValLeuGluArgCysArgGluLeu 90
QY      1601 GGCTGTCTTACAGACATGTGACGAGGATCCGAGGTCGAAAGCCACGCTAGATGATCCAG 1660
Db      91 AsnLeuThrGluArgCysLeuGluLeuProSerArgSerAlaThrLysAspGluIleu 110
QY      1661 ACAAGTCACTTGAATACAC---ACCCTGCTTATGAGACCAAGTCCCTC----- 1708
Db      111 ArgLeuHisThrGluGlnHisPheGluArgLeuValGlyHisSerGlyIleArgAspAsp 130
QY      1709 ---AACGGCAGAGATGACAGACAGAAATGTTCTGCTCCATCAGCCAGAAAGATGAT 1765
Db      131 GluArgMetGluGluLeuSerSerArg----- 139
QY      1766 GCTGTGCTCTGTTGGGGGACATCGGGGTGACAGATGACACCGTGTGAAATGATGAC 1825
Db      140 -----TyrAspSerIleTyrIleHisProSer 148
QY      1826 TCCTCCAGTGTGTGGGATGACATGAGTGGGCTGCTGTGATGATGATGATGATGATGATGAT 1885
Db      149 ThrPheGluLeuSerLeuLeuAlaSerGlySerThrIleGluLeuValAspHisLeuVal 168
QY      1886 GCAGAGACATCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1945
Db      169 AlaGlyLysAlaGlnAsnIleMetAlaIleIleArgProProGlyHisHisValMetCys 188
QY      1946 TCCACAGCATGAGATGTGCTTCTTCAACTGTGTAACATCAACGCAAAATCTCTACAG 2005
Db      189 AlaGluTyrAsnIleTyrCysPhePheAsnValAlaLeuAlaThr-----Gln 205
QY      2006 CAGAAATGAACTGTGGGCAAG-----GTCTCATGTGGAGCTGGAGCATTCACAT 2056
Db      206 HisAlaLeuAspValHisValLeuGlnArgIleLeuIleIleAspTyrAspValHisHis 225
QY      2057 GGCAATGGACCCAGACAGCGATTTCTACAAATGACCCCTGTGCTTACATCTCTGATGAT 2116
Db      226 GlyGlnGlyThrGlnArgPhePheTyrAsnAspProArgValAlaValTyrHisSerIleHis 245
QY      2117 CGTATGACACCGGAATCTTTTCCAGGCTCTGGGCTCTGAA-----GAGGTGTGT 2170
Db      246 ArgPheGlnHisIleLysPheThrProHisValHisGluSerAspTyrHisAlaIleGly 265
QY      2171 GGAGACACAGCGCTGGGGTACAAATGACGTG-----GCATGAGACAGGA 2215
Db      266 SerGlyAlaGlyThrIleTyrAsnPheAsnValProLeuAsnAlaThrGlyMetThrAsn 285
QY      2216 GGTGTGAGACCCCGCATGGAAGCGTGAAGCTTACAGCTTCAAGACAGAGTGTGATG 2275
Db      286 Gly-----AspTyrLeuAlaIlePheGlnGlnLeuLeu 297
QY      2276 CCCATGCCCAC---GAGTTTCACTGATGTGTGCTTCAATGCTCCGCGGGTTGATGCT 2332
Db      298 ProGlyGly***TyrLysPheGlnProGluLeuIleIleValSerValGlyTyrAspAla 317
QY      2333 GTTGAAGACATGTGTCTCTCTGGGTGCTACTGTGTACCGCCAGAGATTTTGGCCAC 2392
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Db      318 AlaleuGly-----CybProGluGlyGluMetGluValThrProAlaCybTy-ProHis 335
Qy      2393 TTGACGACGAGCATGAGACCTTGCGAGGGCCGGGTGGTGGCCCTCGAGGAGGAGCC 2452
Db      336 LeuLeuAnProLeuLeuAlaGlyLeuAlaSerPalAaGValAlaValLeuGluGly 355
Qy      2453 CATGACTTGAACCCGATCTGTGATGCTGAGCTTGAGCTTGCTGGCTGGCTGAGTGA 2512
Db      356 TyrcyLeuAnSerLeuAlaGluGlyAlaAlaLeuThrLeuAaGserLeuLeuGlyAa 375
Qy      2513 AAGTCGACGCTTGTGATGAGGAGCTTTCGAGCAAAACCCCAATCAACGACGAGCC 2572
Db      376 ProCybProProLeuValGluThrVal-----ProLeuProAaGAlaGluLeuAlaGln 393
Qy      2573 ACGTTAAGAAATCATCGATCCAGACCAAACTGAGCTGTGGCCAG 2623
Db      394 AlaleuLeuSerCybAlaAlaValHisAaGProHisThrPaaCybLeuGln 410

RESULT 12
US-09-502-540-15627
; Sequence 15627, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15627
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-502-540-15627

Alignment Scores:
Pred. No.: 1,296-26 Length: 341
Score: 515.00 Matches: 125
Percent Similarity: 50.98% Conservative: 57
Best Local Similarity: 35.01% Mismatches: 115
Query Match: 9.63% Indels: 60
Gaps: 12

US-09-502-945-2 (1-2885) x US-09-902-540-15627 (1-341)
Qy      1481 ACCCAAGTGTGCTACGACACCTTCAAGCAACCAAGTCATGTGCGGAAACA 1540
Db      3 SerThrLeuLeuLeuThrAspProLeuPheGlnHisAspProGlyGlnGly----- 20
Qy      1541 CAGTCGACCCCTGAGCATGCTGCGCGATCCAGACGATCTGTCCCGGCTGACAGACA 1600
Db      21 -----HisProGluSerProSerArgLeuArgGlyLeuGlyValLeuAlaSerThr 38
Qy      1601 GGCCTGCTTACGACGTCGACGCGATCCGAGT-----CGCAAGCC 1642
Db      39 -----ProVallyleGlyThrValMetThrAlaProArgSerAla 51
Qy      1643 ACGTTAATGATCCAGACGATGCTGTAATACACACCCCTGCTTATGGAACAGT 1702
Db      52 ThrGluAlaGluLeuAlaSerValHisThrPro-----GluLeuLeuAlaTyrrLeuGln 69
Qy      1703 CCCCTCAAC-----CGCAGAGAGCTAGACAGCAAGAGTGTCCGATCCATCAGCCAG 1756
Db      70 ArgTlleAnGlyHisAaGAlaGlnHisProAspThrGlnValSerPro----- 86
Qy      1757 AAGATGTATGCTGTGCTGCTTGTGGGGGACATCGGGGTGACAGTGAACCGTGTGAA 1816
Db      86 ----- 86

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Qy      1817 GAGATGCACTCTCCAGTGTGTCGCGATGAGCAAGTGGCTGCTGTGAGACTGCGCTTC 1876
Db      87 -----AspSerValAspAlaAlaAaGLeuAlaAlaGlyAlaSerValGlnAlaValGlu 104
Qy      1877 AAGTGGCTGACAGAGAGCTCAAGATGATTTGGCATCTCGGCCCCAGACACCAC 1936
Db      105 AlalaMetIleGlyGluAlaAaGAnGlyPheAlaLeuValAlaArgProProGlyHisHis 124
Qy      1937 GCGGAGAAATCCACAGCCATGGATTTGCTTTCAACTCTGAGGACATCACCGCAAA 1996
Db      125 AlaGluProAspIleValAlaMetGlyPheCybLeuTyrrHisAsnAlaAlaIleAlaGlu 144
Qy      1997 CTCCTACAGCAGAGATTGAACGTGGGCAAGTCTCTCATCGTGAATGAGCATTCACCA 2056
Db      145 -----AlaGlyArgIleGlyLeuGlyAlaGluArgValLeuValLeuAspThrPaaValHisHis 163
Qy      2057 GGCATGACCAACCCAGCAGGCGTTCTCAATGACCCCTGTGCTTCAATCTGTGCAT 2116
Db      164 GlyAnGlyThrGlnAlaAlaPheThrSerArgAaGAspValMetTyrrGlnSerValHis 183
Qy      2117 CGCTATGACAAAGGAATCTTTCCAGCTCTGGGGCTCTGTAAGAGTTGTGAGAGA 2176
Db      184 GlnPhePro-----TyrrPheProGlyThrGlyAlaAlaProGluValGlyValGly 200
Qy      2177 CCAGGCGTGGGTATCAATGTGACGTGACATGACAGAGAGTGTGACCCCCCATTTGA 2236
Db      201 AlaGlyGluGlyTyrrThrIleAsnValGlyLeuProGlyGly-----AsnSer 216
Qy      2237 GACGTGAGTACCTTACAGCCTTCAGACAGGTGATGCCATTTGCCACGAGTTCTCA 2296
Db      217 AspAlaAspTyrrGlyMetIlePheGluGluLeuLeuProValAlaGluAlaTyrrArg 236
Qy      2297 CCTGATGTGCTTACGCTCCGCGGTTGATGCTGTGAAGACATCTGTCTCTCTG 2356
Db      237 ProGlnLeuIleLeuValSerAlaGlyPheAspSerHisGln-----His---AspProIle 254
Qy      2357 GGTGGCTACTCTGTGACCGGCGATGTTTGGCCACTTGACCAAGCAGCTGATGACCTG 2416
Db      255 GlyGlyMetAspValSerGluArgGlyPheAlaAlaMetCybSerAlaMetIleSerLeu 274
Qy      2417 GCAAGG-----GGCCGGGTGGTCTGCGCTTGAGGAGGAGCCATGATGACC 2464
Db      275 AlaAspSerValCysGlnGlyArgLeuValLeuLeuLeuGluGlyTyrrSerLeuGlu 294
Qy      2465 GCCATCTGTATGCTTGAAGCTTGTGTCTCGGCTTGTCTCAAGTGAAG 2515
Db      295 GlyLeuSerGlnSerValHisAlaCybValGluValLeuAlaGlyArgIle 311

RESULT 13
US-09-248-796A-15279
; Sequence 15279, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15279
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15279

Alignment Scores:
Pred. No.: 4,426-24 Length: 386

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Sequence 18033, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18033
LENGTH: 630
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18033

Alignment Scores:
Pred. No.: 5,71e-22 Length: 630
Score: 447.00 Matches: 191
Percent Similarity: 36.58% Conservative: 72
Best Local Similarity: 26.56% Mismatches: 246
Query Match: 8.36% Indels: 210
DB: 4 Gaps: 28

US-09-502-945-2 (1-2885) x US-09-252-991A-18033 (1-630)
QY 604 CTTCCCGAAGCTGTCAGACAGCAGAGCCGAGAGCCCTCCAGTCCCTGCG 660
DB 27 LeuProValAla-----GlyArgProSerGlyProAlaValAlaVal 41
QY 661 GCAAGGTGACCGCTGACCGCAATTGATGACACATCTCTATTCTGCTGCTGCT 720
DB 42 AlAGly-----LeuProGlnTyrGlnProAla 50
QY 721 GGGCGTGGCAGTGGAGGCGGAGCCCGGAGCCGCTGCTGCTGCTGCTGCTGCT 780
DB 51 -----SerGlySerProArgGlnTyrArgArgGlySerLeu----- 62
QY 781 GCTGTTGTCGAGCAGAGCCGCGGAGCAGACACCTGATGCTGTCGACATCCA----- 834
DB 63 AlAThrlAGlYrGlnAlAGlyTyrProArgArgAlaHisLeuLeuTyrGlnProGlnArg 82
QY 835 -----CGGAGAGTCCCGCACTAGTGAACGGGTGAACGTGTGCGCCAG----- 876
DB 83 ArgValAerLeuHisArgArgHisArgArgArgGlyAerArgGlyAerArgGlnArg 102
QY 877 -----CATGCGAGCGT----- 888
DB 103 ArgGlyThrArgArgArgHisProAerGlyHisArgArgGlyLeuArgLeuHis 122
QY 889 AGGCAAGCTCCCGGAGCAGCCGCGGAGCAGACACCTGATGCTGTCGCGGAGAG 948
DB 123 ArgGlnProProAlaHis-----ArgProAer-----AlaHisArgArg 135
QY 949 TCCCGAGGC-----CTGCAAGCAGCTGCTGATGCAACAGCAGCAGCA 993
DB 136 LeuProGlyAerGlyArgGlyAerProProAlaAerArgProAlaThrAlaGlyAlaLeu 155
QY 994 GTTCTGGAAGAACAAGCAGCAGCAGTACAGCTGGGAGCAAGTCTTCAACAGACAG 1053
DB 156 ArgProGlyArgAlaAlaVal-GlnVal----- 164
QY 1054 GAGAGTCCGAGCAGCAGCAGCAGCAGCAGTGAAGAGAGAGAGAGAGAGAGAGAG 1113
DB 165 -HisLeuAerLeuArgArgProAlaHisPro-ArgLeuProArgArg----- 179
QY 1114 GCAGAGAGCTTCTGCGGAGAGAGAGCCTGACCATGCCCCGAGAGGCTCA----- 1166
DB 180 -----ProGlyProGlnLeuArgProProAerGlnAla 189

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QY 1167 -----CAGAGATGAGACACACAGAAAGACCTGAGAGAGAGAGCA 1209
DB 189 rGleuGlnProGlyHisArgArgArgAlaGlyHisArgProGlyAlaGlyArgThrThr 209
QY 1210 GGAAGAGATGGGAGAGAGAGAGAGATTCATCCAGTTAGAGACAGAGAGCGGAGAG 1269
DB 209 isArgArgGlnArgArgPheProProAlaHisArgArgArg-ArgProGlyArg- 227
QY 1270 TGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1329
DB 227 ----- 227
QY 1330 AGATGCCAAGCCTGCACTTTCAGGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1389
DB 228 -----ProLeuAlaHisArgGlyProGlyLeuPro----- 237
QY 1390 GCCCGCAAGAGCCCTGGGCGGTACCCATCTCCCTGCG----- 1428
DB 238 AlAThrlLeuArgProPheProGlnProArgGlnProAlaMetThrArgArgThrAlaPhe 257
QY 1429 -----TGCCTGGGGGAGTGAAGAACCCCGGAGACCAAGAGAGAGAGAGAG 1473
DB 258 PhePheAerGlyLeuArgGlyLeuTyrPheHisAlaAlaGlyPro----- 270
QY 1474 CTTCTTCAACCAAGGTGTGCTGACGACAGCTTCACTGCTTAAGACACAGTGCATGTCGG 1533
DB 271 -----HisAlaLeuThrLeuProValGlyGlyTyrTrpValGlnProProAlaHisAla 287
QY 1534 GAACACACAGTGCACCTTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
DB 288 GlyHisAlaGlySer-ProGlnThrArgArgGlyLeuSerLeu-----LeuAs 304
QY 1594 GAGACAGGCTCTTGAAGAGTGCAGAGCGAGATCCAGAGTCCGAAGAGCAGTAAAGA 1653
DB 304 PValSerGlyLeuThrAlaArgLeuGlnLeuArgSerAlaProProAlaSerArgGlyAs 324
QY 1654 GATCCAGACAGTGCATGATACCAACACCTGCTGATGAGACAGTCCCTCAACCG 1713
DB 324 PLeuLeuArgValHisProAlaHisTyrLeu----- 334
QY 1714 GCAGAACTAGACAGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1773
DB 335 -----GluArgPheLeuHisLeuSe 341
QY 1774 GCTTGTGGGGGAGTGGGGGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 1833
DB 341 rAerAlaGlyGlySerLeuGlyGlnArgAlaProGlyPro---GlySerTyrGln 360
QY 1834 TGGTGGCGGATGAGTGGGCGGCTGCGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 1893
DB 360 uHisAlaArgLeuSerAlaGlyLeuAlaHisAlaHisAlaHisAlaHisAlaHisAla 380
QY 1894 GCTCAAGAAATGATTTGCTCATCTCCGCGCCCGGAGACACAGCCGAGAGATTCACAG 1953
DB 380 uHisAlaArgLeuAlaTyrSerLeuSerArgProProGlyHisHisLeuProAerGlnAl 400
QY 1954 CATGGATTTCTGCTTTCATCTGTAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 2013
DB 400 aMetGlyPheCysPhePheHisAlaHisAlaHisAlaHisAlaHisAlaHisAlaHis 420
QY 2014 GAAGTGGGAGAGAGTGCATGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 2073
DB 420 rGlyValGlnArgValAlaHisLeuAerTrpAerValHisHisGlyHisHisGlnHis 440
QY 2074 GGGCTTCAAGTGAAGACCCCTGTGCTTACATCTTGTGATGCTATGATGATGATGATGAT 2133
DB 440 aHisTyrTyrArgArgArgArgArgArgArgArgArgArgArgArgArgArgArgArg 458
QY 2134 CTTCTTTCAGAGTCTGCGGCTCTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2193
DB 458 sPheProProGlyTyrSerGlyAlaGlnHisArgGlnArgGlnArgGlnArgGlnArg 478

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Oy		2194	TGTGAAGCTGGCATTGACAGAGAAGGTGGTGAACCCCGCATTTGGAAACCGTGAGTACCTTAAC	2253
Dd		478	lleudsnvalPro-----LenulePrroglYclYclYlHvsmrAlatYlmeGl	494
Oy		2254	AGCCTTCAGACAAGTGTGATATGCCCACTTGGCCSAGAGTTCTCACCTGATGTGTGCSTAGT	2313
Dd		494	nAlamcrlnArgIeValIeuProAlaIeuGlunhArgheArProGlnIleuAlVa	514
Oy		2314	CTCCGCGCGGGTTTGATGCTGTGTGAAGACATCTGTCTCTTGGGTGGCTACTCTGAC	2373
Dd		514	IAlaserIylpheAspAla-----AasnAlaValAspProleuAlaArgmetGlnLeuHl	532
Oy		2374	CGCCGAGATGTTTTGACACTTGACAGACAGACATGATGACCCTG-----GCAG	2421
Dd		532	sSerperSerPheaArgAlaMetThnAlaMetIlleArgAspAlaAlaGlunhArgHlsAlaGl	552
Oy		2422	GCGCCGGGTGGTGTGCTGCGCCTTGAGAGGAGGACCATGACTTGACCGGCACCTGTGTGATGCCTC	2481
Dd		552	YglYArgIeuValValHlsGlunGlYlTyx-----Se	564
Oy		2482	TGAAGCTTGTGTC-----TGCGCTTGCTGAC	2508
Dd		564	rGlunAlaTyxValP::oPhecysgIlyLeuAlaValIlleGlunIleuSerGlyValArgse	584
Oy		2509	TGTAAAGCTGACGCGCTTGATGAGGAGCCTTGACGAAAAAGGCCAAC	2557
Dd		584	rAlaValArgAspProleuArgAspPheIleGlunIeuInmIinProban	600

GenCore version 5.1.6  
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## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 30.8712 Seconds

(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-3

Perfect score: 2140  
Sequence: 1 ggcctgcgtgaacgacgcgcga.....gaagaagaagaagaagaaaa 1298

## Scoring table:

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2\_1/USPTO.spool\_p/US09502945/runat\_10032005\_164737\_13306/app\_query.faeta.1.10979  
-DB=Issued\_Patents\_AA -QPMT=faetan -SUPTX=mar9.ra1 -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdl  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTMT=ptco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09502945\_0CGN\_1.1.283\_@runat\_10032005\_164737\_13306 -ICPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -MSG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued\_Patents\_AA.\*  
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2: /cgn2\_6/prodata/1/1aa/5B COMB .pep.\*  
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6: /cgn2\_6/prodata/1/1aa/backfile1 .pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401	18.7	434	1	US-08-097-830E-3 Sequence 3, Appl1
2	401	18.7	434	2	US-08-456-112B-3 Sequence 3, Appl1
3	368	17.2	608	4	US-09-270-767-32937, A Sequence 32937, A
4	368	17.2	608	4	US-09-270-767-48154 Sequence 48154, A
5	365.5	17.1	235	4	US-09-270-767-36681 Sequence 36681, A
6	365.5	17.1	235	4	US-09-270-767-51898 Sequence 51898, A
7	341.5	16.0	283	4	US-09-270-767-39894 Sequence 39894, A
8	341.5	16.0	283	4	US-09-270-767-55111 Sequence 55111, A
9	326	15.2	71	4	US-09-513-999C-6221 Sequence 6221, Ap
10	313	14.6	611	4	US-09-216-393B-81 Sequence 81, Appl
11	298	13.9	1898	1	US-08-056-200-94 Sequence 94, Appl
12	298	13.9	1898	2	US-08-800-644-94 Sequence 94, Appl

13	298	13.9	1898	4	US-09-538-092-1280 Sequence 1280, Ap
14	291	13.6	411	4	US-09-270-767-41978 Sequence 41978, A
15	281	13.1	735	4	US-10-164-595-80 Sequence 80, Appl
16	281	13.1	784	4	US-10-164-595-79 Sequence 79, Appl
17	281	13.1	843	4	US-10-164-595-54 Sequence 54, Appl
18	272	12.7	919	4	US-09-949-016-6954 Sequence 6954, Ap
19	269	12.6	1240	4	US-09-538-092-658 Sequence 658, Appl
20	265	12.4	1002	2	US-08-460-890A-62 Sequence 62, Appl
21	265	12.4	1003	2	US-08-167-641C-62 Sequence 62, Appl
22	265	12.4	1003	3	US-08-460-891A-62 Sequence 62, Appl
23	265	12.4	1003	3	US-08-462-040-62 Sequence 62, Appl
24	264	12.3	178	4	US-09-489-039A-8236 Sequence 8236, Ap
25	261	12.2	1507	3	US-08-929-329-5 Sequence 5, Appl1
26	256.5	12.0	779	4	US-10-164-595-56 Sequence 56, Appl
27	256.5	12.0	1388	4	US-09-949-016-10817 Sequence 10817, A
28	253.5	11.8	1382	4	US-09-171-991-9 Sequence 9, Appl1
29	252	11.8	309	4	US-09-270-767-46030 Sequence 46030, A
30	247.5	11.6	500	4	US-09-949-016-7692 Sequence 7692, Ap
31	247.5	11.6	712	4	US-09-949-016-10600 Sequence 10600, A
32	246	11.5	793	4	US-09-538-092-1271 Sequence 1271, Ap
33	243	11.4	176	4	US-09-270-767-61576 Sequence 61576, A
34	243	11.4	226	4	US-09-270-767-41210 Sequence 41210, A
35	243	11.4	236	4	US-09-270-767-56426 Sequence 56426, A
36	242.5	11.3	1402	4	US-09-248-796A-14503 Sequence 14503, A
37	240.5	11.2	182	4	US-09-489-039A-8301 Sequence 8301, Ap
38	240	11.2	170	4	US-09-248-796A-27838 Sequence 27838, A
39	239.5	11.2	1564	4	US-10-144-198-4 Sequence 2, Appl1
40	239.5	11.2	1564	4	US-10-144-198-4 Sequence 2, Appl1
41	239	11.2	212	4	US-09-252-991A-19925 Sequence 19925, A
42	239	11.2	1020	4	US-09-538-092-911 Sequence 911, Appl
43	238.5	11.1	447	4	US-09-171-991-4 Sequence 4, Appl1
44	235.5	11.0	171	4	US-09-489-039A-8235 Sequence 8235, Ap
45	234.5	11.0	432	2	US-08-933-750C-47 Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-08-097-830E-3  
Sequence 3, Application US/08097830E  
Patent No. 5652211  
GENERAL INFORMATION:  
APPLICANT: Porro, Massimo  
TITLE OF INVENTION: Peptides For Neutralizing The  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Hedman, Gibson & Costigan, P.C.  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,830E  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Costigan, James V.  
REGISTRATION NUMBER: 25,669  
REFERENCE/DOCKET NUMBER: 576-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 302-8989  
TELEFAX: (212) 302-8998  
INFORMATION FOR SEQ ID NO: 3:



[illegible][illegible]

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Db      447  seglugluuarglyealagluuargarglyseglugluuargargglugluu 467
Qy      1037  GGAAGAAC-----AAGAAAAAGTNAAGAAAGAAAGAAAGAAAGAAAG 1090
Db      467  sargargglugluuarglyseglugluuargglugluuargglugluu 487
Qy      1091  AGAAGAACTAGAGAGAAAGAGAGAAAGAAAGAAAGAAATTAAGACNAGAAAG 1150
Db      487  gargglugluuarglyseglugluuargglugluuargglugluuargglu 507
Qy      1151  AAGAGAGAAAGAAATTAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAGG 1210
Db      507  gglugluuarglyseglugluuargglugluuargglugluuarggluglu 527
Qy      1211  A-----GAAAGAGAGAAAGAAAGAAAGAAAGAAAGTAAAGAA 1246
Db      527  ylysbarglyseglugluuargglugluuargglugluuarggluglu 547
Qy      1247  GCGGAAGAAAGAAAGAAAGTAAAGAGAGAAAGAAAGAAAGAAAG 1296
Db      547  sglugluu-gluargargglugluuargglugluuargglugluuargarg 563
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RESULT 5
US-09-270-767-36681
; Sequence 36681, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36681
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Drosophila melanogaster
US-09-270-767-36681
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Alignment Scores:
Pred. No.: 6,92e-28 Length: 235
Score: 365.50 Matches: 89
Percent Similarity: 58.53% Conservative: 38
Best Local Similarity: 41.01% Mismatches: 62
Query Match: 17.08% Indels: 28
DB: 4 Gaps: 5
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US-09-502-945-3 (1-1298) x US-09-270-767-36681 (1-235)

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Qy      659  AGAAGAGCAAGATGCGAGAGAGAGGCTCGGAGCTCGAGTCTACTA 718
Db      7  lybargglyysalagluasegluvalysegglugluuarglyseglu 26
Qy      719  TGAGGCCAAGGCTCGAAGAGAGAAATCNAAGTTAAAGTATCAAAAGTCGTAA 778
Db      27  ArgGlyserGlyVallysegllylysbargargargCys-----lysbarglu 44
Qy      779  GAAAGAAAGGCCAAGAAAGCCCTAAAGAGTTGAGCAGCTGCGAAGGTTAATCAGC 838
Db      45  gllyluargglyglugluuargglugluuargglu----- 55
Qy      839  TGCCGACTAGAAAGCA-----AGAAAAAGAGAAAGAAAGAGAGAAAGAA 889
Db      56  ---ArgThrlysbarg-Arggllylysegluyllysbargglugluuargglu 74
Qy      890  GAAAGCAAGAGAGAGAAAGAAAGAGAGAGAGAGAGAAAGAAAGAGAGAG 949
Db      74  ylysbglugluuarglyseglugluuargglugluuargglu----- 86
Qy      950  AAGAGAAAGAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009
Db      74  ylysbglugluuarglyseglugluuargglugluuargglu----- 86
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Db      87  -lyseglugluuargarglysegluarglysbargbaengluuyllyseargarggl 106
Qy      1010  TAAAGAGAGAGAGAGAAATTAAGAGAGAAAGAAAGAAAGAAAGTNAAGAGAGAG 1069
Db      106  uylsegluyllysbarglysegluyllysbargglugluuyllysbarggluglu 126
Qy      1070  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129
Db      126  uylsbarglysegluarglyse-----Argbaengluuyllyseargarggl 142
Qy      1130  GAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
Db      142  uylsegluyllysbarglysegluyllysbargglugluuyllysbarglyseglu 162
Qy      1190  GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1249
Db      162  elysbargargglugluuargglugluuargglugluuyllysbargglugluuylly 182
Qy      1250  GAAAGAGAGAGAGAGAGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1298
Db      182  glylysegluyllysbarglysegluargglugluuargglugluuyllyse 198
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RESULT 6
US-09-270-767-51898
; Sequence 51898, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51898
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Drosophila melanogaster
US-09-270-767-51898
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Alignment Scores:
Pred. No.: 6,92e-28 Length: 235
Score: 365.50 Matches: 89
Percent Similarity: 58.53% Conservative: 38
Best Local Similarity: 41.01% Mismatches: 62
Query Match: 17.08% Indels: 28
DB: 4 Gaps: 5
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US-09-502-945-3 (1-1298) x US-09-270-767-51898 (1-235)

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Qy      659  AGAAGAGCAAGATGCGAGAGAGAGGCTCGGAGCTCGAGTCTACTA 718
Db      7  lybargglyysalagluasegluvalysegglugluuarglyseglu 26
Qy      719  TGAGGCCAAGGCTCGAAGAGAGAAATCNAAGTTAAAGTATCAAAAGTCGTAA 778
Db      27  ArgGlyserGlyVallysegllylysbargargargCys-----lysbarglu 44
Qy      779  GAAAGAAAGGCCAAGAAAGCCCTAAAGAGTTGAGCAGCTGCGAAGGTTAATCAGC 838
Db      45  gllyluargglyglugluuargglugluuargglu----- 55
Qy      839  TGCCGACTAGAAAGCA-----AGAAAAAGAGAAAGAGAGAGAGAGAAAGAA 889
Db      56  ---ArgThrlysbarg-Arggllylysegluyllysbargglugluuargglu 74
Qy      890  GAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 949
Db      74  ylysbglugluuarglyseglugluuargglugluuargglu----- 86
Qy      950  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009
Db      87  -lyseglugluuargarglysegluarglysbargbaengluuyllyseargarggl 106
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Dd	108	uglucglutylserglythrargylserglucglutylserlle***lyselyselysgluar	128
Oy	1117	-----AGAAAAGAAGAAAGCAATAAAGAACAAAGAAAGGAAGAAAG	1165
Dd	128	g**Argglylutylserysglutlu--lyselyselsglutylysarglyselysarglyls	147
Oy	1164	AATTAAGACGAGAAAGAAAGAAAGAGAA-----	1192
Dd	148	Arglysergluatrylsrglulysrarglyserglutluencluartrylsargglutluartrylsels	167
Oy	1194	-----AGAAAGGAAAGAAAGAGAAAAAGAAAGAAAGAAAGAAAGT	1243
Dd	168	lyselyselglyalrarglylsrarglyselglylucgluatrarglyserglutylselyselgu	187
Oy	1242	AGAAAGCGGAAGAAAGAAAGAAAGTATTAGAAAGCAGAAAGAAAGAAAGAAAGAA 1298	
Dd	188	Arggluartrylsrargglutlutls-----lyselglyselyselysglyglutuls 204	
RESULT 8			
US-09-270-767-55111			
; Sequence 5511, Application US/09270767			
; Patent No. 6703491			
; GENERAL INFORMATION:			
; APPLICANT: Homburger et al.			
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster			
; FILE REFERENCE: File Reference: 7326-094			
; CURRENT APPLICATION NUMBER: US/09/270.767			
; CURRENT FILING DATE: 1999-03-17			
; NUMBER OF SEQ ID NOS: 62517			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 55111			
; LENGTH: 283			
; TYPE: PRT			
; ORGANISM: Drosophila melanogaster			
; FEATURE:			
; OTHER INFORMATION: Xaa means any amino acid			
US-09-270-767-55111			
Alignment Scores:			
Pred. No.: 1.82e-25 Length: 283			
Score: 341.50 Matches: 82			
Percent Similarity: 66.17% Conservative: 51			
Best Local Similarity: 40.80% Mismatch: 36			
Query Match: 15.96% Indels: 32			
DB: 4 Gaps: 6			
US-09-502-945-3 (1-1298) x US-09-270-767-55111 (1-283)			
Oy	780	AAAGAAAGGCCCAAGAAAGCCCTTAAGAGTTTAGACAGCTGCCGAAGGTTAATTCAGCT	839
Dd	10	lyselglylserglutylsrglyalrarglyselyselglutlutlylsrlylsrlylsrlyls	29
Oy	840	GCCGCACCTAGAAGACGAAGAAAGAAAGAGAAAGAGCAGACGAGAAAG-----AAG	890
Dd	30	glulysrarglyglutylsrlsrglutylsrglutuartrylsrarglyserglutlutlyls	49
Oy	891	AAGAAACAGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA	950
Dd	50	lyselysels***Arglylsrargglutlutylselysrgr-glutlutylsrsrarglysrgr	69
Oy	951	AAGGAAGAGAGAAAGAAAGAAAGAGAAAGAAAGAAAGAAAGAGAAAGAA-----	1002
Dd	69	srgglyllyselyselglylserglutuartrylgluartrylsrarglylsrlylsrlylsr	89
Oy	1003	-GAAGAACTAAGAAAGAGAGAGAAAGTAATTAAGAGAAAGAAAGAAAGAAAGTNNAA	1061
Dd	89	ulyselysluartryglutlutlylsrlylsrlylsrlylsrlylsrargglutylsrglyls-	108
Oy	1062	GAAGAAAGAAAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-	1116
Dd	108	ugluglutylserglutlylrargtrylsrglucglutlutylserlle***lyselyselysgluar	128
Oy	1117	-----AGAAAAGAAGAAAGAAATTAAGCAACAAAGAAAGAAAGGAAGAAAG	1165

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Db      128 g***ArgGlyGluIuylsYlsGluGlu--LysYlsYlsGluGluYlsArgYlsArgYls 147
Oy      1164 AATAAGAGAGCAAGAAAGAAAAGAGAAA----- 1193
Db      148 ArgYlsGluArgYlsGluYlsArgYlsGluYlsGluYlsArgYlsArgYlsArgYlsYls 167
Oy      1194 -----AAGAGAGAGAAAGAGAAAGAAAGAAAGAAAGAAAGT 1241
Db      168 LysYlsGluYlsArgYlsYlsArgYlsGluYlsGluYlsArgYlsGluYlsGluYls 187
Oy      1242 AGAAAGCGTAAGAAAGAAAGAAAGTATAGAGAGAGAGAGAGAGAGAGAGAGAG 1298
Db      188 ArgGluArgYlsArgYlsGluYls-----LysGluYlsYlsYlsGluYls 204

RESULT 9
US-09-513-999C-6221
; Sequence 6221, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6221
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6221

Alignment Scores:
Pred. No.:          3,77e-24          Length:          71
Score:              326.00             Matches:          68
Percent Similarity: 95.77%             Conservative:     3
Best Local Similarity: 95.77%           Mismatches:      0
Query Match:        15.23%             Indels:          0
DB:                  4                  Gaps:           0

US-09-502-945-3 (1-1298) x US-09-513-999C-6221 (1-71)

Oy      11  ATGACTGGGAACCGGCTTGCAGAGAGCCTTGTGCTTGGCCANCAAGAAAGTAACTAGCG 70
Db      1  MetThrAlaAsnA-GLeuAlaGluSerLeuLeuAlaLeuSerGlnGlnGluLeuAla 20
Oy      71  GATTTCGCAAAAGACTACTCTTGTAGAGTGAAGTGAAGTGAAGGCGGCAATGATGAGAG 130
Db      21  AspleuProYsaAepYrLeuLeuSerGlnSerGluAspGluYlsAspAenAepGlyGlu 40
Oy      131 AGAAGACATCAAAACCTTCTGGAAGCAATCACTTCCCTTGATGAAAGATAGCGGAGAA 190
Db      41  ArgYlsHsGlnYlsLeuLeuGluAlaLeuSerSerLeuAspGlyYlsAsnArgYls 60
Oy      191 TTGGCTGANNAGTCTGAGGCTAGTCTGAAGGTG 223
Db      61  LeuAlaGluArgSerGluAlaSerLeuYlsVal 71

RESULT 10
US-09-216-393B-81
; Sequence 81, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERE
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B

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: CURRENT FILING DATE: 1998-12-18
: PRIOR APPLICATION NUMBER: 08/994,825
: PRIOR FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 366
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 81
: LENGTH: 611
: TYPE: PRT
: ORGANISM: Toxoplasma gondii
US-09-216-393B-81

Alignment Scores:
Pred. No.:      1,666-22      Length:      611
Score:          313.00      Matches:     100
Percent Similarity: 45.52%      Conservative: 103
Best Local Similarity: 22.42%      Mismatches:  154
Query Match:    14.63%      Indels:      89
OB:             4          Gaps:        11

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[illegible]

[illegible]

[illegible][illegible]













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Db      1589 SerGlnSerLeuMetValProGlnSerGlySerProGluProGluSerIleArgAsnThr 1608
QY      62 GGTGCGACACGACGAGCTGACCTGGCCACGACATGACCGAAGAGCCCGAGAAAT 121
Db      1609 SerArgSerSerThrProAlaIlePheAla-Ser---AspProAlaThrCysProIle11 1627
QY      122 TCCGGCATAGAGTGATTTTCTGATTGAAATGATGC----- 158
Db      1627 eProGly-----CysGluThrThrIleGluIleSerIy 1638
QY      159 ----AGAGAGGACTATCTCTATGATGTGCTG----- 186
Db      1638 sglYArgThrGlyLeuGlyLeu-SerIleValGlyIleYSerAspThrLeuLeuGlyAla1 1658
QY      187 -----CGAATGTACACACAG-----ACCATGACGCGCGCGCTGCTG 226
Db      1658 IeIleIleHnIsgluValIlyrGluGluGlyAlaAlaCysIysAspGlyArgLeuTrpAlaG 1678
QY      227 GAGACCTGAACCTGCTCATCAAT----- 249
Db      1678 IyAspGlnIleLeuGluValAsnGlyIleAspLeuArgIysAlaThrHleAspGluAla1 1698
QY      250 -----GAAACCAAGCCGTCTGCTCTGTTTGAATGCCATTGCGCCGCTGA 292
Db      1698 IeAsnValIeuArgIlnThrProGlnArgValArgLeu---ThrLeuYrArgAspGlu1 1717
QY      293 TCCCACTGACAGACACAGGTGAATATGATGACGTGACGTCGCGCGCGCTCAGAGAGCTGA 352
Db      1717 IabProYrIyysGluGluGluValAlCysAspThrLeuThr----- 1729
QY      353 AGGAGGTGCGCTCTGACCGCTGTGACCCCGAGAGCGCTGCGCTGAGTGTGCTGCGCC 412
Db      1730 ----IleGluLeuGlnIyIysIyPheGlyIySerGlyLeuGlyIleValGlyIysA 1748
QY      413 TGGAGTTTGCGCTTGGGCTTTTATCTCCCACTCATCAAGGCGGTGACGGCAGACAGCG 472
Db      1748 rgsAn---AspThrIyValPheValSerAspIleValIyysGlyIyIleAlaAspAlaA 1767
QY      473 TCGGG---CTCCAGTAGAGGAGACGAGATGCTCCGGAATGATGATTTTCATCCCTCC 529
Db      1767 sptIyArgLeuMetGlnIyAspGlnIleLeuMetValAsnGlyIyGluAspValArgAsnA 1787
QY      530 GTACCCATGAGAGAGTGTATCAACCTCATTCGA---ACCAAGAAAGCTGTGTCATCAAG 586
Db      1787 IathrGlnIyValIyValAlaIleLeuLeuIyysCysSerLeuGlyThrValThrLeuGluV 1807
QY      587 TGAAGACATCGGCTGATCCCGGTGAAAAGCTTCTCTGATGACCCCTCATTTGGCAGT 646
Db      1807 aI-----GlyArgIleIyValIySerSerThrSerGluSerLeu----- 1820
QY      647 ATGTGATCATGTTTGTGTGGGATCTGGGGCGTGGAGGACACCTGGGCTCC-----C 700
Db      1821 -----GlnSerSerSerIyIysAsnAlaIleAlaIleAsnGluIleG 1834
QY      701 CTGGAATCGGGAACAAAGAGAGAGAGCTTTTCATCAAGCTGTAGAGCTCCCGAGGCC 760
Db      1834 IngIyLeuArgThrValGluMetIyIys-----GlyProThrAspSerI 1849
QY      761 TTGGCTGACGACATTTCCAGCGGC-----CCCATCCAGAAAGCTGGCATCTTTATCA 811
Db      1849 eucIyIleSerIleAlaIyGlyIyValGlySerProLeuGlyAspValProIlePheIleA 1869
QY      812 GCCATGGAAGACGAGCTGCTGCTGCTGAGAGG---GGATTGGAGATAGGGAGACAG 868
Db      1869 IatMetCethIspromIyValAlaIleGlnThrGlnIyIyLeuArgValGlyIyAspArgI 1889
QY      869 TTGTGCAAGTCAATGAGCTGACCTTCTTCACTGATCATCAAGAGAGGCTGTAAATGTGC 928
Db      1889 IeValIThrIleCySglYThrSerThrGluIyMetThrIethrGlnAlaValAsnLeu 1909
QY      929 TGAATAATAGCCGCGAGCTGACCATCTCATTTAGCTGACGTGCGGAGAGCTGTTCA 988

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Db      1909 euIyAsnAla---SerGlySerIleGluMetGlnValAlaIyGlyAspVal----- 1926
QY      989 TGACAGACCGGAGCGGCTGACAGAGCGCGGACGCTGAGCTGACCGGACGACTTC 1048
Db      1927 -----SerValValThrGlyHnIsglnGlnIyProIleAsnSerSerLeuS 1942
QY      1049 TCATGCAAGAGCGGCTGCGATGAGACTCCAAACAATCTCTCCAGAGACAGAGAGATGG 1108
Db      1942 eRPh-----ThrGlyLeuThrSerSerSerIlePheGln----- 1953
QY      1109 AGCGGCAAGAGAAAGAAATTTGCCAGAGACAGAGAAATGAGATACCGGA 1168
Db      1953 ----- 1953
QY      1169 AGGAGATGGAACAGATTGTAGAGAGAGAGAGAGATTGAAGACAAATGGAAGAACT 1228
Db      1954 -----AspAsp 1956
QY      1229 GGGGCTCAAGAAAGACGTAATCTTGTGCTTAAACATCACTGCTGATACCCAGTAC 1288
Db      1956 euGlyProProGln-----CysIySerIleThrLeuGluArgIyPro----- 1970
QY      1289 CCTTGGCAAGCAAGTATGATCAGGAGTGGAACTGAGCTCGAGCCGCGAGATGACC 1348
Db      1970 ----- 1970
QY      1349 TGGATGAGAGCAGCAGAGAGAGAGAGAGAGATTCCGAAATATGAGAAAGCTTTG 1408
Db      1971 --AspIy----- 1972
QY      1409 ACCCTTAATCTATTTACCCCAAGACAGATCATGSGGAGAGATGTCGGGCTCTAGCA 1468
Db      1972 ----- 1972
QY      1469 TCAAGAAAGAGGAGATCCTTGAACCTGCGCCGTGGAAGCGGTGAGCTCCCATTTGG- 1527
Db      1973 -----LeuGlyPheSerIleValGlyIyIyYrGlySerProHnIyA 1987
QY      1528 ----AAGTGTGCTTGTCTGCTGTGTATGACGCGGAGCTGTGACCGGACATGTGGA 1582
Db      1987 spleuProIleYrValIyThrValPheAlaIySglIyAlaIleAsnGluAspGlyArgI 2007
QY      1583 TTGTGAAGGGGACGAGATCATGCAATCAACGCGAAGATTGTGACAGACTACACCTGG 1642
Db      2007 euIyAspGlyAspGlnIleIleAlaValAsnGlyIySerLeuGluIyValThrHnIeG 2027
QY      1643 CTGAGGCTGACGCTGCGCTGCGAGAG 1668
Db      2027 IuGluAlaValAlaIleLeuIyAsp 2035

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## RESULT 2

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US-09-306-998-3
; Sequence 3, Application US/09306998
; Patent No. 6291173
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavligian, Sean V.
; TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC2
; CURRENT APPLICATION NUMBER: US/09/306,998
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 60/084,740
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-306-998-3

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Alignment Scores: 2.18e-13 Length: 2037
Pred. No.:

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Score: 267.50 Matches: 142  
Percent Similarity: 35.81% Conservative: 109  
Best Local Similarity: 20.26% Mismatches: 223  
Query Match: 6.49% Indels: 228  
DB: 3 Gaps: 26

US-09-502-945-4 (1-2236) x US-09-306-998-3 (1-2037)

QY 388 CTGGGCTAGTGTGGCTGGCTGGAGTTGGCTGTGGCTTTGATCTCCACCTC 447  
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1018 LeuGlyMetThrValSerAlaMetLeuValSerPheGlyLeuGlyMetLeuValAlaGlySerLeu 1036  
QY 448 ATCAAGGCGGTAGGACAGACAGCTGCGG---CTCAGAGTAGGAGGAGATGCTGCGG 504  
DB |||:|||||  
1037 LeuGlyValAlaLeuSerArgPheGlyArgLeuAlaLeuGlyMetLeuValSerLeuSer 1056  
QY 505 ATCAATGATATTTCATCTCTCTCTGATCCCATGAGAGGATCAACCTCATTCGAAAC 564  
DB |||:|||||  
1057 IleAsnGluSerThrIleSerValThrAsnAlaGluAlaArgAlaMetLeuValArg--- 1075  
QY 565 AAGAAACTGTCTCCATCAAGTAGACACATCGGCTGATCCCGTGAAGAGCTCTCT 624  
DB |||:|||||  
1076 ---ArgHis---SerLeuIle---GlyPro 1082  
QY 625 GATGAGCCCTCACTTGG---CAGTATGTGATCAGTTGTGTCGATCTGGG 675  
DB |||:|||||  
1083 AspLeuIleValIleThrValProAlaGluHisLeuGluIlePheValIleSerLeuGly 1102  
QY 676 GCGCTGCGAGGCGCTG--- 693  
DB |||:|||||  
1103 GluGlnSerGlyArgValMetAlaLeuAspPhePheSerSerThrGlyArgAspPhe 1122  
QY 694 ---GCTCCCTCGAATCGGGAACAGAG--- 723  
DB |||:|||||  
1123 ProGluLeuProGluArgGluGluGluGluGluSerGluLeuGluAsnThrAla 1142  
QY 724 ---AAGAGGTC 732  
DB |||:|||||  
1143 TyrSerAsnThrAsnGlnProArgArgValGluLeuThrArgGluProSerLeuValSerLeu 1162  
QY 733 TTCATCAGCTGTAGAGCTCCGAGGCTTGGCTGAGCATTTCCAGCGGCCCATCTCAG 792  
DB |||:|||||  
1163 GlyIleSerIleValGlyArgGlyMetGlySerArgLeuSerAsnGlyValMet 1182  
QY 793 AAGCTGGCATCTTTATCAGCCCATGTGAACCTGGCTCTGTCTGTGAGGCTGGA--- 849  
DB |||:|||||  
1183 Arg---GlyIlePheIleLeuValIleValLeuGluAspSerProAlaGlyAsnGlyThr 1201  
QY 850 TTGGAGATAGGGGAGCCAGATTGTGSAATGAGGCGGTGAGCTTCTTAACCTGAGATCAC 909  
DB |||:|||||  
1202 LeuLysProGlyAspArgIleValGluValAspGlyMetAspLeuArgAspAlaSerHis 1221  
QY 910 AAGGAGCTGTAAATGTGTAATAATATAGCCGAGCTGACCTTCATCTGATTTAGCTGCA 969  
DB |||:|||||  
1222 GluGlnAlaValGluAlaIleArgLysAlaGlyAsnProValAlaPheMetValGlnSer 1241  
QY 970 GCTGCGCGGAGCTGTTCATGACAGACCGGAGCGCTGCAAGGCGCGGACGCTGAG 1029  
DB |||:|||||  
1242 ---IleIleAsnArgProArgAlaProSerGlnSerGlnSerGln 1255  
QY 1030 CTGCAGCGGAGAGCTTCTCATGACAGAGCGGCTGGCGATGAGTCCACCAAGATCTTC 1089  
DB |||:|||||  
1256 ProGluLysAlaProLeuVal--- 1262  
QY 1090 CAGGAGCAGAGAGAGGAGCGGCAAGAGAAAGAAATTCGCCAGAGAGCAGAG 1149  
DB |||:|||||  
1263 ---SerAlaProProProProProSerAlaPheAlaGluMetGlySerAsp 1278  
QY 1150 GAAATGAGAGATACCGGAGAGAGATGAAACAGATTGTAGAGAGAGAAAGTTTAAG 1209  
DB |||:|||||  
1279 HisThrGlySerSerAlaSerValIleSerGlnAspValAspGluValAspGluPheGly 1298  
QY 1210 AAGCAATGGGA---GAAAGCTGGGGGCTCAAGAGAAAGCAAGTACTTGGCTTAA 1260

DB |||:|||||  
1299 TyrSerThrPheValAsnIleArgGluArgGly--- 1309  
QY 1261 ACCATCACTGCTGAGTACACCCAGTACCCCTTCCGAG--- 1299  
DB |||:|||||  
1310 ThrLeuThrGlyGluLeuHisMetIleGluLeuLysGlyHisSerGlyLeuGlyLeu 1329  
QY 1300 ---CCA 1302  
DB |||:|||||  
1330 SerLeuAlaGlyValAsnLysAspArgSerArgMetSerValPheIleValGlyIleAspPro 1349  
QY 1303 AAGTATGATCAGAGAGTGAACCTGAGCTGACCCCGACAGATGACCTG---GAT 1353  
DB |||:|||||  
1350 AsnGlyAlaAlaGlyLysAspGlyArgGluGlnIleAlaAspGluLeuGluIleAsn 1369  
QY 1354 GGA---GGCAGAGAGAGCAGGAGAGCAGAGATTTCCGAAA--- 1392  
DB |||:|||||  
1370 GlyGlnIleLeuThrGlyArgSerHisGlnAsnAlaSerSerIleIleLysCysAlaPro 1389  
QY 1393 ---TATGAGAAAGCTTTGAC 1410  
DB |||:|||||  
1390 SerLysValLysIleIlePheIleArgValAsnLysAspAlaValAsnGlnMetAlaValCys 1409  
QY 1411 CCCTACTATTGTTCAACCCA---GAGCAGATCATGGGAAAGATGTC 1455  
DB |||:|||||  
1410 ProGlyAsnAlaValAlaGluProLeuProSerAsnSerGluAsnLeuGluAsnLysThr 1429  
QY 1456 GCGCTCTTACGATCAAGAAAGAGGATCTTACCTGACCTGCGCTG--- 1500  
DB |||:|||||  
1430 GluProThrValThrThrSerAspAlaAlaValAspLeuSerSerPheLysAsnValGln 1449  
QY 1501 ---GAAAGCGGTG---GACTCCGCC 1521  
DB |||:|||||  
1450 HisLeuGluLeuProLysAspArgGlnGlyLeuGlyIleAlaIleSerGluAspThr 1469  
QY 1522 ATGGAGAGGTGCTGTTCTGCTGTATGACCGGAGCTCTGAGCGGATGTGTC 1581  
DB |||:|||||  
1470 LeuSerGlyValIleLeuLysSerLeuThrGlnHisGlyValAlaAlaThrArgLysArg 1489  
QY 1582 ATTTGAAAGGGGAGCAGATCATGAGATCAACGCGAAGTTGTGACAGACTACACCTG 1641  
DB |||:|||||  
1490 LeuLysValGlyAspGlnIleLeuAlaValAspAspGluIleValValGlyTyrProIle 1509  
QY 1642 GCTGAGGCTGAGCTGCGCTGCGAGAGGCTGGAATCAGGCGGAGCTGATGACCTT 1701  
DB |||:|||||  
1510 GluLysPheIleSerLeuLeuLysThrAla--- 1519  
QY 1702 GTGGTTCGCTGCGCCCGCAAGAGATGACATGACCTGACTTTGCTGA---GTC 1760  
DB |||:|||||  
1520 ---LysMetThrValLysLeuThrIle 1527  
QY 1761 CAAGAGGAGAACCAATTCACGCTTAGAGAAACAGTACCTCCGCGCCACCTGTGA 1820  
DB |||:|||||  
1528 HisAlaGluAsnProAspSerGlnAlaValProSerAlaIleAlaLysArgGlyGlu 1547  
QY 1821 CAGAAAGCTCGGACAGACCTTAGAGAGGCGCATGACACACAGCAGATGCACTTGG 1880  
DB |||:|||||  
1548 LysLysAsnSerSerGlnSerLeuMetValPro---GlnSerGlySerPro 1563  
QY 1881 GAGCTGAATCTATTC---ACCCAGAAATCTCAACTCC---TTGGCCCTGAA 1928  
DB |||:|||||  
1564 GluProGluSerIleArgAsnThrSerArgSerSerThrProAlaIlePheAlaSerAsp 1583  
QY 1929 CCA--- 1931  
DB |||:|||||  
1584 ProAlaThrCysProIleIleProGlyCysGluThrThrIleGluIleSerLysGlyArg 1603  
QY 1932 ---GGGCGAGATAAAGAACAGCTGGGCGCATTTTGA 1967  
DB |||:|||||  
1604 ThrGlyLeuGlyLeuSerIleValGlyGlySerAspThrLeuLeuGluAlaIleIle 1623  
QY 1968 AGGCAATGTGAGAGAGAGAGCAGCAGCCGTTGGAGAAAGATCTCAAGATCCAGA 2027  
DB |||:|||||

[illegible]

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Oy      781   GGCCCAATCCAGAAACCTGGCATCTTTTAACAAGCATTG-----AAACCGGTCC    831
Db      373   Gtgcgt---Aargtgytguglytlepheileserphelleualaglyglyprolalaasp    391
Oy      832   CTGTCTGTCTGAAGTGGGATTGGAGATAGGGGACACAGATTGTGCMAATGACGCTTCAC    891
Db      392   Leustergtgcgtgltcgt---LeuaatrgylglYasproinlleuservaleahnglyValaasp    409
Oy      892   TTCTTAACTTGATCACAAAGAGACTGTAAATGTCTGAATAAATAGCCGACCTGCACC    951
Db      410   Leuatrgenaalaserthleaglucinalaalallealeuleuyasenalia---GlyglnThr    428
Oy      952   ATCTCCATTGTACGTGCAGCTGCCGGGGAGCTGTTCATGCACAGACCCGGAGCGGCTTGCA    1011
Db      429   Valthrillelleallagin-----TyrlyseProglugluTyrseryarphe    443
Oy      1012   GAGGCGGCGGACGCTGAGCTGCACGCGGACGAGCTTCTCATGCGAAGACGCTGGCATG    1071
Db      444   Gluaialayvliehlaerpleuaatrglugln-----LeumetanserserleuglySer    461
Oy      1072   GAGTCCAAACAAGATTCTCCACAGAACACAGAGAG-----ATGAGC    1110
Db      462   GlythrilaaserleuaxgerserAmprolyearglytyrIleakgalaleupheasp    481
Oy      1111   CGGCAAGAGAAAAGAATTTGCCACAGAAGCGACACAGAAAAATGAGATACCGGAG    1170
Db      482   TyrArpyrVthrylvaaPcyeglyPhelauseerlinalauseerPheacgrPheglyAsp    501
Oy      1171   GAGATGGAACAGATTGTTAGAGAGAGAAAGAAAGATT-----    1206
Db      502   ValleuhilvalilleapralaserAepdgluglutrrpttrpglnalaaagvalyahisier    521
Oy      1207   -----MAGAACAA    1215
Db      522   AerpsergiuthtaarparilleglyPheileproserlyuaragarValaGluaaxargclu    541
Oy      1216   TGGGAA-----GAAGATCGGGGCTCA-----MAGAA    1242
Db      542   TrpearlagleulyalaalybaasprtpglYserxserglyseringilyatrgluasp    561
Oy      1243   CAGCACTCTTGCCTAAACCATCACT---GCTGAGGTACAC-----CCAGTACC    1290
Db      562   SerValleuserTyrgluthinhvalthhgImecsluvahnlyTrylalaaqprollaile    581
Oy      1291   CTTGCGAAGCCAAAGTATGATCAGAGGAGTGAACCTGAGCTCGAGCCCGCAGATGACTG    1350
Db      582   lleueuglyrrothrllyvaarpargdalaaahmaasrlyeuseusergiunPheroproalye    601
Oy      1351   GATGGAGCGACSGAGAGACSGAGAGACAGAGATTCCGGAATATGAGAAAGCTTTGAC    1410
Db      602   PhegllyserCyvalaProhilethThraBrgprolyuarvaguTyrgluilleaerdylyaxg    621
Oy      1411   CCCATCTATNTGTCACCCCSAGACSAATATGAGGGAAGATGTCGGGCTCCTAACGATC    1470
Db      622   AspyrthiarphevaliserSeraatrglylwmetoishuysarplieglinalanhlysrPhe    641
Oy      1471   AAGAAGAGAGGAGCTTTAGACTGCGCCCTGGAGAGCGAGTGTGACTCCCCATT-----    1524
Db      642   lileguialeglygnlyrdaanserhialeuTyrglyrhgservalginserValaarglu    661
Oy      1525   -----GGGAAG-----GTGTCCTTTTCTGCTGTGTATGACGG    1557
Db      662   ValaiaagluglnjlylvnhlsCytleleudarvaliserlaalenalivalaaxargleu    681
Oy      1558   GGAGCTGTGAGCGGCAATGCTGGCATTTGT-----AAAGGAGACGATC    1602
Db      682   GlmlaiahlanyleuhlaeproillaallepheilleatrgProayrgserleuGluaAenvAl    701
Oy      1603   ATGGCAATCAAACGCAAGATTGTGACAGACTACACCTGGCTGAGCTGACGCTGCC    1659
Db      702   leugluilleahenyvatrglllethnrgluglnglnlaaryglusalarephaargla    720

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[illegible][illegible]

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FILE REFERENCE: MMSCL Gene
CURRENT APPLICATION NUMBER: US/09/233,086
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: US 60/071,861
EARLIER FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 05
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1881
TYPE: PRF
ORGANISM: Homo sapiens
US-09-233-086-3

Alignment Scores:
Pred. No.: 9,77e-13 Length: 1881
Score: 259.50 Matches: 149
Percent Similarity: 37.03% Conservative: 115
Best Local Similarity: 20.90% Mismatches: 232
Query Match: 6.30% Indels: 217
DB: 3 Gaps: 31

US-09-502-945-4 (1-2236) x US-09-233-086-3 (1-1881)
QY 85 CCTGGCCCGAGCCCTGGACCGGAAAGTGGCCCGGAAATCCGGCATAGGTGATTTCTG 144
DB ||||| |||||
DB 169 ProGlySerValAlaAspArgAsp-----GlnArgLeu 179
QY 145 ATTGAATATGATCAGAGAAAGACTATCTATGATGTGTCGAATGTACACAGACC 204
DB ||||| |||||
DB 180 LysGluAsnAsp-----GlnIleuAlaIleAsnIleThrPro 192
QY 205 ATGAGC-----GTGGCCGTGCTC-----GTGGAGAC 221
DB ||||| |||||
DB 193 LeuAspGlnAsnIleSerHisGlnGlnAlaIleAlaIleuGlnGlnThrGlySer 212
QY 232 CTGAAGCTGTATC---AATGAACC-----AGCCGTGCTCTG 270
DB ||||| |||||
DB 213 LeuArgLeuIleValAlaArgGluProValHisThrLysSerSerThrSerSerLeu 232
QY 271 TTGTATGCATTTGGCGCTGATCCCATGAAACACACAGGTGAATATGATCAGTGACC 330
DB ||||| |||||
DB 233 AsnAspThrThrLeuProGluThrValCysTrpGlyHisValGluGluValGluLeuIle 252
QY 331 CCCCGGCGCTCCAGAAAGCTGAAGAGAGTGCTGTGACCGCTGACCCCGAAGCCTTC 390
DB ||||| |||||
DB 253 AsnAspGlySer-----GlyLeu 258
QY 391 GGCCTTAGTGTGCGTGGTGGCTGTGAGTTGGCTGTTCATCTCCACCTCATC 450
DB ||||| |||||
DB 259 GlyPheGlyIleValGlyGlyLysThr-----SerGlyValValValArgThrIleVal 276
QY 451 AAAGGCGGTACAGGACAGAGCTCGGG---CTCCAGTAGGGAGAGAGATCGTCCGATC 507
DB ||||| |||||
DB 277 ProGlyGlyLeuAlaAspArgAspGlyArgLeuGlnThrGlyAspHisIleLeuValIle 256
QY 508 AATGATATTCATCTCTCTCTGACCATGAGAGGTGATCAACCTCATTCGAAACC--- 564
DB ||||| |||||
DB 297 GlyGlyThrAsnValIleGlnGlyMetThrSerGluGlnValAlaGlnValIleuArgAsnCys 316
QY 565 AAGAAACTGTCTCCATCAAGTGAAGACACATCGGCTGATCCCGTGAAAGACTCTCT 624
DB ||||| |||||
DB 317 GlyAsnSerValArgPheLeuValAlaArgAspProAlaGlyAspIleSerValThrPro 336
QY 625 GATGACCCCTCACTTGGCAGTATGTGATCAGTTTGTGCGGAATCTGGGCGGTGCGA 684
DB ||||| |||||
DB 337 ProAlaProAlaAlaIleuProValAlaIleuProThrValAlaSerLysGly----- 353
QY 685 GGCAGCTGGGCTCCCTGTGAATTCGGGAAACAAAGAGAAAGAGTCTTCATCAGCCTG 744
DB ||||| |||||
DB 354 -----ProGlySerAspSerSerLeuPheGluThrTrpAsnValGluLeu 368
QY 745 GTA-----GGCTCCGAGGCTTGGCTGGCAGACATTTCCAGCGGC 783
DB ||||| |||||

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DB 369 ValArgLysAspGlyGlnSerLeuGlyIleValGlyIleValGlyIleValGlyIleThrSerHis 388
QY 784 CCCATCCAGAAAGCTGGCATTTTATACCCATGTGAACCTGGCTCCCTGTCTGTG 843
DB ||||| |||||
DB 389 ThrGlyGluAlaSerGlyIleTrpValLysSerValIleProGlySerHisIleValArgHis 408
QY 844 GTGGGA---TTGAGATTAAGGACCGAGTGTTCGAAGTCAATGGCTTCATCTTAAAC 900
DB ||||| |||||
DB 409 AsnGlyHisIleGlnValAsnAspLysIleValAlaValAspGlyValAsnIleGlnGly 428
QY 901 CTGATCACAAGAGCGCTTAAATGTGCTGAATAATAGCCGACCTGACCATCTCCATT 960
DB ||||| |||||
DB 429 PheAlaAsnHisAspValAlaGluValIleuArgAsn----- 440
QY 961 GTAGCTGACCTGGCCGAGAGCTTTCATGAC----- 993
DB ||||| |||||
DB 441 -----AlaGlyGlnValValHisLeuThrLeuValArgArgLysThrSerSer 457
QY 994 -----GACCCGAGCGGCTGGCAGAGCGCGGACGCTGAG 1029
DB ||||| |||||
DB 458 ThrSerProLeuGluProProSerAspArgGlyThrValValGlu-----Pro 473
QY 1030 CTGCAGCGGACGAGCTTCTCATGCAAGACGCGCTGCGCATGGATCAAGATCTTC 1089
DB ||||| |||||
DB 474 LeuLysProProAlaLeuPheLeuThrGlyAlaValGluThrGluThrAsn---ValAsp 492
QY 1090 CAGAGACACAGAGATGAGAGCGGCAGAAAGAAATATGCCAGAAAGCAGCAGAG 1149
DB ||||| |||||
DB 493 GlyGluAspGluGluIle-----LysGluArgIleAspThrLeuLysAsn 507
QY 1150 GAAATGAAGATATCCGGAAGAGATGAACACAGATTGTGAAGAG---GAAAGAAAGTTT 1206
DB ||||| |||||
DB 508 AspAsnIleGlnAlaLeuGlnLysLeuGlnLysValProAspSerProGluAsnGluLeu 527
QY 1207 AAGAACCAATGGGAAGAAGACTCGGGCTCAAGGAACACTTCTTCCCTTAACCATC 1266
DB ||||| |||||
DB 528 LysSerArgTrpIleuAsnLeuLeuGlyProAspTrpGlyValMetValAlaThrLeuAsp 547
QY 1267 ACTGCTAGAGTACACCCAGTACCCCTTCGAAAGCCAAATGATGATCAG----- 1314
DB ||||| |||||
DB 548 ThrGlnIleAlaAspAspAlaGluLeuGln-----LysTyrSerLysLeuLeuProIle 565
QY 1315 -----GAGTGAACCTGAG----- 1329
DB ||||| |||||
DB 566 HisThrLeuArgLeuGlyValGluValAspSerPheAspGlyHisIleTrpIleSerSer 585
QY 1330 -----CTGAGCCCGCAGATGACCTG--- 1350
DB ||||| |||||
DB 586 IleValSerGlyCysProValAspThrLeuGlyLeuLeuGlnProGluAspGluLeu 605
QY 1351 -----GATGGA----- 1356
DB ||||| |||||
DB 606 GluValAsnGlyMetGlnLeuTrpGlyLysSerArgGluValAlaSerPheLeuLys 625
QY 1356 ----- 1356
DB 626 GluValProProProPheThrLeuValCysCysArgArgLeuPheAspGluAlaSer 645
QY 1357 -----GGCAGGAGAGAGCAGGAGAGCAG 1380
DB ||||| |||||
DB 646 ValAspGluProArgArgThrGluThrSerLeuProGluThrGluValAspHisIleAsnMet 665
QY 1381 GATTTCCGGAATATGAGAAAGCTTTGACCCCTCATGTATGTTCAACCCGAGAGATC 1440
DB ||||| |||||
DB 666 AspValAsnThrGluGluAspAspArgGlyGluLeuAlaLeuThrSerProGlu----- 683
QY 1441 ATGCGGAGAGATTCGGGCTCTCAAGCATCAAGAGAG-----GGAATCTTA 1488
DB ||||| |||||
DB 684 -----ValLysIleValGluLeuValLysAspCysLysGlyLeuGlyPheSer 699
QY 1489 GACGTGCGCTGGAAGCGGTGTGACCTCCCATTTGGAAGAGTGTGCTTGTGCTG 1548
DB ||||| |||||
DB 700 IleLeuAspTrpIleAspProLeuAspProThrArgSerValIleValIleArgSerLeu 719

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QY 1549 TATGAGCGGAGCTCTGAGCGCATGTGCATTGTGAAGGAGGAGCATCATGCA 1608  
DB 720 ValAlaAspGlyValAlaGluArgSerGlyGlyLeuLeuProGlyAspArgLeuValSer 739  
QY 1609 ATCAACGGCAGATTGTGACAGACTACACCTGTGGAGGCTGACGCTGCTGACAG 1668  
DB 740 ValAlaGluGlyCysLeuAspAsnThrSerLeuAlaGluAla---ValGluIleLeuLys 758  
QY 1669 GCGTGAATCAGGCGGAGCATGATGACCTTGTG---GTGCGCTGCTGCCCCCA--- 1722  
DB 759 AlaValProProGly-----LeuValHisLeuGlyIleCysValProLeu 773  
QY 1723 ---AAGAGATGACGATGAGTGTGACCTTGTGCTG-----AAG 1758  
DB 774 ValGluAspAsnGluGluSerCysTrpIleLeuHisSerSerSerAsnGluAspLys 793  
QY 1759 TCCAAAGGAGGAAACCAATTCAAGGCTTAGAAACAGT 1797  
DB 794 ThrGluPheSerGlyThrIleHisAspIleAsnSerSer 806  
RESULT 6  
US-09-562-737-21  
/ Sequence 21, Application US/09562737  
/ Patent No. 6428967  
/ GENERAL INFORMATION:  
/ APPLICANT: Herz, Joachim  
/ APPLICANT: Gotthardt, Michael  
/ TITLE OF INVENTION: LDL Receptor Signaling Pathways  
/ FILE REFERENCE: USM0708  
/ CURRENT APPLICATION NUMBER: US/09/562,737  
/ NUMBER OF SEQ ID NOS: 132  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 21  
/ LENGTH: 724  
/ TYPE: PRF  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: Sequence  
US-09-562-737-21  
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Best Local Similarity: 23.26% Mismatches: 200  
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US-09-502-945-4 (1-2236) x US-09-562-737-21 (1-724)

QY 610 GTGAAAAGCTCTCTGATGAGCCCTCACTTG---CAGTATGTGATCATGTTGTCTG 666  
DB 254 SerTrpAlaProProAspIleThrThrSerTrpSerGlnHisLeuAspAsnGluIleSer 273  
QY 667 GAATTCGGGGCGGTGAGGAGCAGCTGGGC--- 696  
DB 274 HisSer-----SerTrpLeuGlyThrAspTrpProThrAlaMetThrProThr 289  
QY 697 -----TCCCTCGAATAATCGGAA-----AACAG 720  
DB 290 SerProArgArgTrpSerProValAlaLysAspLeuLeuGlyGluAspIleProArg 309  
QY 721 GAGAAAGAGTCTTCAACAGCTGTGATGCTCCCGAGGCTGTGAGCATTTCCAGC 780  
DB 310 GluProArgArgIleValIleHisArgGlySerThrGlyLeuGlyPheAsnIleValGly 329  
QY 781 GGGCCCATCAAGAGCCTGGCATCTTTATCAGCATGTG-----AACTGCTCC 831  
DB 330 GlyGlu---AspGlyGluGlyIlePheIleSerPheIleLeuAlaGlyGlyProAlaAsp 348  
QY 832 CTGCTGCTGAGTGGATGATGAGATGAGGAGCAGATGCTGCAAGTGCATGCGCTGAC 891  
DB 349 LeuSerGlyGlu-----LeuArgLysGlyAspGlnIleLeuSerValAsnGlyValAsp 366  
QY 892 TTCTTAACCTGATCAACAAGAGCTGTAAATGCTGTAATAATGAGCCGACCTGACC 951  
DB 367 LeuArgAsnAlaSerIleGluGlnIleAlaIleAlaLeuLysAsnAla---GlyGlnThr 385  
QY 952 ATCTCAATGTAGCTGACAGCTGGCGGAGAGCTGTTCATGACAGACCGGAGCGGCTGGCA 1011  
DB 386 ValThrIleIleAlaGln-----TyrLysProGluGluTrpSerArgPhe 400  
QY 1012 GAGCGCGGAGGCTGAGCTGACGCGGAGGAGGAGCTTCTCATGCAAGAGCGGCTG--- 1065  
DB 401 GluAlaLysIleHisAspLeuArgGluGln-----LeuMetAsnSerSerLeuGlySer 418  
QY 1066 -----GCGATGAGTCCAAC----- 1080  
DB 419 GlyThrAlaSerLeuArgSerAsnProLysArgGlyPheTrpIleArgAlaLeuPheAsp 438  
QY 1080 ----- 1080  
DB 439 TyrAspLysThrLysAspCysGlyPheLeuSerGlnAlaLeuSerPheHisPheGlyAsp 458  
QY 1081 -----AAGATCTCCAGAGCAGCAGAGATGAGCGGCAAGAAAGAAATTGCC 1134  
DB 459 ValLeuHisValIleAspAlaSerAspGluGluTrpTrpGlnAlaArgArgValHisSer 478  
QY 1135 CAGAAAGCAGCAGAGAAATGAGAGATACCGGAAAGAGATGGAAGATTGTAGAGAG 1194  
DB 479 AspSerGluThrAsp-----AspIleGlyPheIleProSerLys 491  
QY 1195 GAAGAGAGTTTAAGAGCAATGGAA-----GAAAGCTGGGGCTCA----- 1236  
DB 492 ArgArgValGluArgArgGluTrpSerArgLeuLysAlaLysAspTrpGlySerSer 511  
QY 1237 -----AAGAACAGCTACTCTTGGCTTAAACCTACT---GCTGAGGTA 1278  
DB 512 GlySerGlnGlyArgGluAspSerValLeuSerTrpGlyThrValIleTrpGlnMetGluVal 531  
QY 1279 CAC-----CCATACCCCTTCCGACAGCCAAATATGATGATGAGAGTGAACCTGAG 1329  
DB 532 HisTrpAlaArgProIleIleIleLeuGlyProThrLysAspArgAlaAsnAspAspLeu 551  
QY 1330 CTGAGCCCGCAGATGACTGTGATGAGGCAAGGAGAGCAGAGAGAGAGATTTCCGG 1389  
DB 552 LeuSerGluPheProAspLysPheGlySerCysValProHisThrThrArgProLysArg 571  
QY 1390 AATATGAGGAAGGCTTTGACCCCTACTATGTTGACCCCAAGAGAGATGAGGGAAG 1449  
DB 572 GlnTrpGlnIleAspGlyArgAspTrpHisPheValSerSerArgGlyLysMetGluLys 591  
QY 1450 GATGTCCGGCTCTTACGATCAAGAGAGGAGTCTTGAAGCTGGCCCTGAGAGCGGT 1509





[illegible]

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Db      414 SerSerLeuGlyLysGlyThraLaserLeuArgSerAsnProLeuArgGlyPheTyrIle 433
QY      1093 -----GAGCAGCAGGATGAG 1110
Db      434 ArgAlaLeuPheMetLysThrLysThrLysAspCysGlyPheAsnSerGlnAlaLeuSer 453
QY      1111 CGGCAAGAGAAACAAATTGCCAAGAGCAGAGAGAAATAGAGATACCGG--- 1167
Db      454 PheHisPheGlyGlnValLeuHisValIleAspAlaSerAspArgGlyLysTrpGlnAla 473
QY      1168 -----AAGGATGAGACAGATT-----CTAAGACAGAGAAAGAAAG 1203
Db      474 ArgArgValHisThrAspSerGlyThrAspAspIleGlyPheValProSerLysArgArg 493
QY      1204 TTAAAGACCAATGG-----GAAGACAGCTGG----- 1230
Db      494 ValGluArgArgTrpTrpSerArgLeuLysAlaLysAspTrpTrpLysSerSerArgLys 513
QY      1231 ---GGCTCAAGAGACAGTACTCTTGCCTAAACATCACT---GCTGAGGTACAC--- 1281
Db      514 GlnGlyArgGlnLysAspValLeuSerTyrGlnThrValThrAspMetGlnValHisTyr 533
QY      1282 -----CCAGTACCCCTTGCAAGCCCAAGATGATCAGGAGAGTGAACCTGCTCGAG 1335
Db      534 AlaArgProIleGlnLeuGlyProThrLysAspArgAlaPheAspAspLeuLeuSer 553
QY      1336 CCGCAGATGACCTGGATGAGGACGACGAGACGAGACGAGAGATTTCCGGAATAT 1395
Db      554 GluPheProAspGlyPheGlySerCysValProHisThrThrHisProLysValArgGlyTyr 573
QY      1396 GAG---GAAGCTTTGACCCCTACTGTATGTTCAACCCAGACAGATCATGGGAAAGAT 1452
Db      574 GluIleAspGlyIleAsp---TyrHisPheValSerSerArgGlyLysMetGlnLysAsp 592
QY      1453 GTCCGGCTCTTACGACATCAAGAGAGGAGATCTTACAGCTGGCCCTGGAAGGC---GGT 1509
Db      593 IleGlnAlaHisLeuLeuIleGlnAlaGlyGlnTyrAsnSerHisMetYrGlyThrSer 612
QY      1510 GTGGAATCCCCC-----ATTGGAAGAGTGTCTGTT 1539
Db      613 ValGlnSerValArgAsnValAlaGlnGlnGlyLysHisCysValIleGlnAspValSerAla 632
QY      1540 TCTGCTGTATGAGCAGGAGCTGCTGAGCGGCACT---GGTGCATTTGAAAGG 1593
Db      633 AsnAlaValAlaArgArgArgGlnAlaAlaHisLeuHisProIleAlaSerPheIleArgPro 652
QY      1594 -----GACGAGATCATGCAATCAACGCAACGCAATTTGTGACAGATACACCTGGCT 1644
Db      653 ArgSerLeuGlnAsnTrpLeuGlnIleAsnLysArgIle-----ThrGlnVal 668
QY      1645 GAGGCTGACGCTGCGCTGCAAGAGCCTGGAATCAAGGCGGAGCTGATGCACTTTG 1704
Db      669 GlnAlaArgLysAlaPheLeuAspArgAlaTrpLysLeuGlnGlnIleuPheThrGlyCysTyr 688
QY      1705 GTTCCGCTC 1713
Db      689 SerAlaIle 691

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RESULT 9
US-09-270-767-42903
; Sequence 42903, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42903
; LENGTH: 533
; TYPE: PRT

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; ORGANISM: Drosophila melanogaster
US-09-270-767-42903
Alignment Scores:
Pred. No.: 9 05e-11 533
Score: 232.50 Matches: 82
Percent Similarity: 42.15% Conservative: 71
Best Local Similarity: 22.59% Mismatches: 114
Query Match: 5.64% Indels: 96
DB: 4 Gaps: 13
US-09-502-945-4 (1-2236) x US-09-270-767-42903 (1-533)
QY      340 TCCAGAGACGTGAAGAGAGGTGCGTGTGACCGCTTGACCCCGAAGGCTTGCGCTGACT 399
Db      190 SerGlyGlnAlaGlnGlnValValLeuProLys---AsnGlnGlySerLeuGlyPheSer 208
QY      400 GTGCGTGTGCGCTGAGCTTGCGCTGT-----GGGCTCTTC 435
Db      209 IleIleGlyGlyThrAspHisSerCysValProPheGlyThrArgGluProGlyIlePhe 228
QY      436 ATCTCCACCTGATCAAGAGCGGTGAGGAGACAGCGTGGG---CTCCAGGTAGGAGAC 492
Db      229 HisSerHisIleValProGlyGlyIleAlaSerLysCysGlyLysLeuArgMetGlyAsp 248
QY      493 GAGATGTCGGATCAATGATGATTCATCTCTCTCTGATCCATGAGAG---GTCAATC 549
Db      249 ArgIleLeuLysValAlaAsnGlnLysValSerLysValAlaThrHisGlnAspAlaValLeu 268
QY      550 AACCTGATTCGAACCAAGAAACGTGTGTCAATCAAAAGTACACATCGGCTGATCCCC 609
Db      269 GluLeuLeuLysProGlyAspGlyLysLeuThrIleGlnHis----- 283
QY      610 GTGAAAGCTTCCTGATGAGCCCTCACTTGACAGATAGTGATCAGTTGTGTGCGAA 669
Db      284 -----AspProLeuProProGlyPheGlnGlnValLeuLeuSerLys 297
QY      670 TCTP-----GGGCGTGTGAGGACAGCTGGCTCC 699
Db      298 AlaGlnGlyLysArgLeuLysMetHisIleLysGlyLysAlaGlnGlyLysAlaGlnGly 317
QY      700 CCTGGAATCGGGAACCAAGAGAAAGAGCTTTCATACAGCTGTAGCTCCGAGGC 759
Db      318 ProAlaAspProSerAspLys----- 324
QY      760 CTTGCTGAGCATTTCCAGCGGCCCATCCAGAACCTGGCATCTTTATCAGCCATGTG 819
Db      325 -----GlyAlaPheValSerLysIle 331
QY      820 AAACCT---GGTCCCTGTCTGTGAGTGGATTTGAGATAGGAGACAGATTTGCA 876
Db      332 AsnSerValGlyAlaAlaArgArgAspGlyArgLeuLysValGlyMetArgLeuLeuGln 351
QY      877 GTCAATGCGGTGACCTTCTTAACCTGATCAACAGAGAGCTTAATGTCTGAAAAAT 936
Db      352 ValAsnGlyHisSerLeuLeuGlyAlaSerHisGlnAspAlaValAsnValLeuAspAsn 371
QY      937 AGCCGAGCTGACCATCTCATTTGATGAGTGAAGTGGCGGAGCTGTTCATGACAGAC 996
Db      372 -----AlaGlyAsnGlnIleGlnLeuVal -Va 380
QY      997 CGGAGCGGCTGAGCAGAGCGCGGACGCTGAGCTGACAGCGGAGAGCTTTCATGACAG 1056
Db      380 LysLysGlyTyrAspLysSerAsnLeuLeuHisSerIleGlyGlnAlaGlyLysMetSer 400
QY      1057 AACGCGCTGCGCATGAGATCCAAAGATCC-----TCCAGAGACAGACAGATGAGAG 1110
Db      400 rThrGlyPheAsnSerAspLysSerCysSerGlyLysSerArgGlnGlySerArgLysIle 420
QY      1111 CGGCAAGAGAAAGAAATTTGCCAAGAGGAGCA-----GAGGAA 1152
Db      420 rGluThrGly--SerIleuSerGlnSerGlnSerValSerSerLeuAspHisGlnGlu 439

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Oy		1153	AATGAGAAATACCGGAGAGAATGGACAGATTGTAGAGGGAGAGAAAGTTTAAGAAG	1212
Dd		440	AapGUAAGLeuAGClnApPheAspValPheAlaSerGln-----LysPro	455
Oy		1213	CAATGGGAAGAAGACTGGGGCTCAAG-----	1238
Dd		456	AapIaGInGlnProThrCdlYProSerValLeuAlaLaLaLaLaMeValHisGly	475
Oy		1240	GAAcAGCTACTTCCTCCATAAACCATCACTGCTGAGTACACCAGTACCCCTTGCAAG	1299
Dd		476	AlaSerSerProThrProProAlaalaThrSerAenIIeThnProLeuProThrAlaala	495
Oy		1300	CCA 1302	
Dd		496	Pro 496	
RESULT 10				
US-09-562-737-23				
; Sequence 23, Application US/09562737				
; Patent No. 6428967				
; GENERAL INFORMATION:				
; APPLICANT: Herz, Joachim				
; APPLICANT: Gotthardt, Michael				
; TITLE OF INVENTION: LDL Receptor Signaling Pathways				
; FILE REFERENCE: UTSW0708				
; CURRENT APPLICATION NUMBER: US/09/562,737				
; CURRENT FILING DATE: 2000-05-01				
; NUMBER OF SEQ ID NOS: 132				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO: 23				
; LENGTH: 724				
; TYPE: PRT				
; ORGANISM: Artificial Sequence				
; FEATURE:				
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic				
US-09-562-737-23				
Alignment Scores:				
Pred. NO.:	2,31e-10	Length:	724	
Score:	228.50	Matches:	123	
Percent Similarity:	39.01%	Conservative:	97	
Best Local Similarity:	21.81%	Mismatches:	207	
Query Match:	5.55%	Indels:	137	
	4	Gaps:	26	
US-09-502-945-4 (1-2236) x US-09-562-737-23 (1-724)				
Oy		340	TCCAGAAAGCTGAMAGAGAGCTGCCTGTGACCGCTGCACCCGAAAGCCTTGGCCTGAGT	399
Dd		155	AAGluGyllellellegllulleleryrilelys--GIYProlYgllYleuglYpheAla	173
Oy		400	GTGCCTGTGGCGCTG-----GAGTTTGCTGTGG-----CTTTATCTCCAC	444
Dd		174	IleaAglylgYvalGlylaSngllnlhsaPrProGlyaPaSaSenSerIetyrValThrlu	193
Oy		445	CTCATCAAGCGGTCCAGAGACAAGCGTGGG---CTCCAGTGGGAGACGAGATCGTC	501
Dd		194	IlelleegluGylYAlaAlahlsYsbheglYla-gleuglnlleGlYasplYslleGly	213
Oy		502	CGGATCAATGATATTCCATCTCTCTGTAACCATGAGAG--GTCAATCACTCAAT	558
Dd		214	AlaValaSaSenSerValGlYleuglnUbaphlsMethlsGluApsAlaValAlaaleuIlle	233
Oy		559	CGAACCAAGAAAACGTGTCTCCATCAAAGTGA-----CACATGGCCTGATCCCCGTG	612
Dd		234	AasnThrTYraSPvaIValTYrlenuYbsYbaLaLYsProSeRaSnAlaTYrlenuSerleu	253
Oy		613	AAAACTCTCCGATGAGGCCCTCACTTGG-----CAGTATGGATCAAGTTGTGCG	666
Dd		254	SerTYrlaAProProaPrlleThrThreTYrSerGlnHlsleuApsAengluIlleAen	273
Oy		667	GAATCTGGGGCGTCCGAGGACCTTGAGC-----	696

Db	274	HisSer-----SerTyrLeuGlyIleThrAspTyrGlnThrAlaMetThrProThr	289
Qy	697	-----TCCCTCGAAATCGGAA-----	720
Db	290	SerProArgSerTyrSerProValAlaIleAspLeuThrGlnGluAspIleProArg	309
Qy	721	GAGAAAGAAAGCTTCATCATCAGCGCTGGTAGGCTCCGAGAGCCTTGCGTCAGATTCCAGC	780
Db	310	GluProArgValIleValIleIleAspGlySerThrIlyTrpGlyPheAsnIleValGly	329
Qy	781	GGCCCGCATCCGAAAGCCTGGATCTTTATGACGCATGNG-----AAACCTGGCTCC	831
Db	330	GlyGlu---AspTyrGlnGlyIlePheIleSerPheIleLeuAspGlyGlyProAlaAsp	348
Qy	832	CTGTCTGCTGAGCTGGAGATTGGAGATGAGGAGACAGATTGCTGAAATGCAATGGCGCTGAC	891
Db	349	LeuSerGlyGlnGlu-----ArgIleGlyIleAspGlnIleLeuSerValPheGlyValAsp	366
Qy	892	TTCTCTTAACCTGGATTCACAGAGAGCGCTGAAATGCTGTAATAATGCTGACCGCAGCTGACC	951
Db	367	LeuArgAsnAlaSerThrIleGlyGlnAlaIleIleLeuIleuAsnAlaIleGln--Thr	385
Qy	952	ATTCGCATTGAGTCGAGCGAGCTGGCGGGAGCTGTCATGACAGACCGGAGCGGCTGGCA	1011
Db	386	ValThrIleIleAlaGln-----TyrIleProGlnGluTyrSerArgPhe	400
Qy	1012	GAGCGCGCGGACGCTGAGCTGACCGCGGAGCGCTTCTGACGAAAGCGGCTGGCGATG	1071
Db	401	GlnAlaLeuIleIleAspLeuAspArgGlnGlnIleuMetIleSerLeuGlySerGlyThr	420
Qy	1072	GAGTCCAAACAGATCTTCCAGAGACACAGAGATGAGCGGCGAAAGAGAAAGAAATT	1131
Db	421	AlaSerIleAspG---SerAspProIleArgGlyPhe	431
Qy	1132	GCCCAAGAAAGGACGAGAGAAATAGAGATACCGGAG-----	1170
Db	432	TyrGlnArgAlaLeuPheAspTyrAspIleThrArgAspCysGlyPheLeuSerGlnAla	451
Qy	1170	-----	1170
Db	452	LeuThrPheIleSerPheGlyAspValLeuIleValAlaAspAlaSerAspGlnGluTrpTrp	471
Qy	1171	GAGATGGAACGATTTGAGAGGAGAAAGAAAGTT-----	1206
Db	472	GlnTrpArgValIleIleSerAspSerGlnThrTyrAspIleGlyPheIleProSerIlys	491
Qy	1207	-----AAGAAAGCAATGGGA-----GAAAGCTGGGGCTCA-----	1236
Db	492	ArgAlaValGluArgAspGlnTrpSerArgIleuAspAlaIleAspIleTrpGlySerSerSer	511
Qy	1237	-----AAGGAACAGCTACTCTTGCTGCTAAACATCACT-----GCTGAGGTA	1278
Db	512	GlyGlnGlnGlyArgGlnAspSerValIleuSerPheGlnThrValIleTrpGlnMetGlnVal	531
Qy	1279	CAC-----CCAGTACCCCTTCGCAAGCGCAAGATGATGATCAGGAGTGGAACTGAG	1329
Db	532	HisGlyAlaArgProIleIleIleLeuGlyProIleIleAspArgAlaAsnAspAspLeu	551
Qy	1330	CTCGAGCCCGGACATGACCTGAGATGAGAGCGACCGAGAGACAGGAGAGACAGATTTCCGG	1389
Db	552	LeuIleGluPheProAspIlePheGlySerCysIleAspProIleIleThrThrArgProIleAsp	571
Qy	1390	AAATATGAGAAAGGCTTGAACCCCTACTGATGTTGACCCCGAGACGATCATGCGGAG	1449
Db	572	GluLeuGlnIleAspGlyIleAspTyrHisPheMetSerSerArgGlnIleMetGlnIleAsp	591
Qy	1450	GATGTCCGGCTCTTACGATCAAGAAAGAGGAGATCTTAGACCTGGCCCTGGAAGCGGT	1509
Db	592	AspAsnGlnAlaIleIleValPheIleGluAlaGlyArgTyrAsnSerHisIleuTyrGlyThr	611
Qy	1510	GTGAGCTCCCATTTGGGAGAGTGGTC-----GTTTCT	1542

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Db      612 SerSerGlnSerValArgGlnValAlaGlnGlnThrLysHisCysIleLeuSerValSer 631
Qy      1543 GCTGTATAGAGCGGAGAGCTGCTGAGCGGCGATGTGGCATTTG----- 1587
      |||||
Db      632 AlaValAlaValArgArgLeuGlnAlaAlaHisThrHisProIleAlaIlePheIleArg 651
Qy      1588 -----AAAGGGAGCAATCATGCGAATCAACGCGAAGATTGTGACAGACTACACCTCG 1641
      |||
Db      652 ProTyrSerLeuGlnValLeuGlnIleAsnAlaArgIleThrGlnGlnAlaArg 671
Qy      1642 GCTGAGGCTGACGCTGCTGCTGCGAAGAGCGCTGGAATCAG----- 1680
      |||||
Db      672 LysAspPheAspArgAlaThrLysLeuGlnGlnPheThrGluCysPheSerAlaIle 691
Qy      1681 ---GGCGGGGAC 1689
      |||||
Db      692 ValGlyGlyAsp 695

RESULT 11
US-09-562-737-26
; Sequence 26, Application US/03562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-26

Alignment Scores:
Pred. No.: 1.08e-09 Length: 724
Score: 220.50 Matches: 126
Percent Similarity: 38.05% Conservative: 81
Best Local Similarity: 23.16% Mismatches: 218
Query Match: 5.35% Indels: 119
Gaps: 24
DB: 4

US-09-502-945-4 (1-2236) x US-09-562-737-26 (1-724)
Qy      346 AAGCTGAAGAGGTGCTCTGACCGTCTGACCCGCGAAGCTCGGCTGAGTGTGCGT 405
      |||||
Db      157 LysIleIleGlnIleLysLeuIleLys---TyrProLysGlnLeuGlnPheSerIleAla 175
Qy      406 GGTGGC-----CTGAGTTTGGCTGTGGGCTTTTCATCTCCACCTTCATC 450
      |||
Db      176 AlaGlyValGlyAsnGlnHisIleProGlnGluAsnSerIleTyrValThrLysIleIle 195
Qy      451 AAGGGGCTGACGAGCAGCGCTCGGGCTC---CAGGTAGGGAGCAGATCGTCCGGATC 507
      |||||
Db      196 PheGlnGlyAlaIleAlaHisLysAspGlyArgGlyGlnIleGlyAspLysIleLeuAlaVal 215
Qy      508 AATGATATTTCATCTCTCTCTGATCCAT---GAGAGGCTCATCAACTCATTTGCAACC 564
      |||
Db      216 HisSerValGlyLeuGlnAspValMetHisIleAspAlaValAlaIleLeuLysAsnThr 235
Qy      565 AAGAAACTGTGTTCACAAAGTGAACACATCGGCTGATCCCGTGAAAAGCTCT--- 621
      |||
Db      236 LysAspValValTyrLeuLysValAlaLysLeuSerAsnAlaTyrLeuSerAspSerTyr 255
Qy      622 -----CTGATAGAGCCCTCACTTG---CAGTATGTGATCAGTTTGTGGGAATCT 672
      |||||
Db      256 MetProProAspIleThrThrSerTyrSerAsnHisLeuAspAsnGlnIleSerHisSer 275
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Qy      673 GGGGGCTGCGAGGACCTGGGCTCC-----CTGCAAAATCGGAAAACAAGAGAG 726
      |||||
Db      276 -----GlnTyrLeuGlnThrAspTyrProThrAlaArgThrProThrSerPro 291
Qy      727 AAGCTTTTCATCAGCTGGTA----- 747
      |||
Db      292 ArgArgTyrSerSerValAlaLysAspLeuGlnGlnThrIleProArgGlnPro 311
Qy      748 -----GGCTCCGAGGCTTGGCTGAGCATTTTCACGGGCCCC 786
      |||||
Db      312 ArgArgIleValValHisArgGlySerThrGlnLeuGlnPheThrIleValGlyGln 331
Qy      787 ATCCAGAACCTGGCATCTTTATACAGCATGTGAAACCTGGC-----TCCTGTCT 837
      |||
Db      332 ---AspGlyGlnGlyTyrPheIleSerPheIleLeuAlaGlyValAlaAlaAspLeuSer 350
Qy      838 GCTGAGCTGGAGTTGGAGATAGAGGACCGAATTTGTGCAAGTCAAGGCGCTGCTCTCT 897
      |||||
Db      351 GlyGlu-----LeuArgLysAspAspGlnIleLeuSerValAsnGlyValGlnLeuArg 368
Qy      898 AACCTGATCACAAGAGGCTGTAAATGTGTGAATAATAGCGGACCTGCACATCTCC 957
      |||
Db      369 AsnAlaSerHisGlnGlnAlaPheIleAlaLeuLysAsnAla---GlyGlnThrGlyThr 387
Qy      958 ATTGTAGCTGCAGCTGGC----- 975
      |||||
Db      388 IleIleAlaGlnTyrLysProGlnHisTyrSerArgPheGlnAlaLysIleHisIleLeu 407
Qy      976 CGGAGCTTTTCATACACACCGGAGCGGCTGGGACGCGGAGCGGAGCTGTCAG 1035
      |||||
Db      408 ArgGlnGlnLeuMetAsnSerSerLysGlySerGlyThrAlaSerLeuArgSerLeuPro 427
Qy      1036 CGGACAGAGCTTCTCATGACAGAACGCGCTGGCGATGACTCCAAACAG----- 1083
      |||||
Db      428 LysArgGlyPheTyrIleArgAlaMetPheAspTyrAspLysThrLysAspCysAsnPhe 447
Qy      1084 -----ATCTCCAGAGACGACGAG 1101
      |||
Db      448 LeuSerGlnAlaLeuSerPheHisGlnGlyAspValLeuHisValIleAspAlaArgAsp 467
Qy      1102 GAGATGACCGGCAAAAGCAAAAGAAATTTGGCCGACAGCAGCAGCAAGAAATAGCAG 1161
      |||||
Db      468 GlnGlnTyrTrpGlnAlaArgArgSerHisSerAspSerGlnThrAspAspIleThrPhe 487
Qy      1162 TACCGGAAAGATAGTGAACAGATTGTAGAGAGGAAGAAAGTTTAAGAACATATGGA 1221
      |||
Db      488 IleProSerLysArgArgValGlnValArgGlnTyrPseArgLeuLysValLysTrp--- 506
Qy      1222 GAAGACTGGGGCTCA-----AAGAAACAGCTACTTTGCTTA 1260
      |||||
Db      507 -----TrpGlySerSerSerGlySerGlnGlyTyrGlnAspSerValLeuSerTyrGln 524
Qy      1261 ACCATACAT---GCTGAGTACAC-----CCAGTCCCTTGGCAAGCCAAAGTAT 1308
      |||||
Db      525 ThrAlaThrGlnMetCysValHisTyrAlaArgAspIleIleLeuGlnProThrLys 544
Qy      1309 GATCAGAGATGAGACCTGAGCTGAGCCCGGACGATGACCTGATGAGAGCAGCAGAGAG 1368
      |||||
Db      545 ArgGlnAlaAsnAspAspLeuSerLeuSerGlnPhePheAspLysPheIleCysValPro 564
Qy      1369 CAGGAGACAGAGATTTCCGAAATATGAGAAAGGCTTTGACCCCTTATCTATGTTCAAC 1428
      |||
Db      565 HisGlyThrArgProLysArgGlnTyrGlnIleHisGlyArgAspTyrHisIlePheValSer 584
Qy      1429 CCAGAGCAATCATGAGGAGATGTCGGGCTCGTACGATCAAGAAAGAGGAGATCCTTA 1488
      |||
Db      585 SerIleGlnLysMetCysLysAspIleGlnAlaLysLysPheIleGlnAlaGlyGlnTyr 604
Qy      1489 GACCTGCGCTGGAGAGC---GATGTGACCTC----- 1518
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Db      605 AsnLeuHisLeuTyrGlyThrSerValGlnSerMetArgGlnValAlaGlnGlnGlnLys 624
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QY 1519 ---CCCATTCGGAGGTGCTGTTCTGCTGTATGAGCGGGAGCTGCTGAGCGGCAT 1575
Db 625 HieAsnIleLeuAaspValSerAlaAsnAlaValGlnArgLeuGlnAlaHisLeuHis 644
QY 1576 GGTGGCATTTGTG-----AAAGGGACGAGATCATGCAATCAACGGCAAG 1620
Db 645 ProArgAlaIlePheIleArgProArgSerLeuSerAsnValLeuGluIleAsnLysArg 664
QY 1621 ATTGTGACAGATPACACCCCTGGCTGAGGCTGACGCTGCCCTGCAGAGGCGCTGGAATCAG 1680
Db 665 IleValGluGluGlnAla-----ArgLysAlaPhe-----674
QY 1681 GCGCGGGAGCTGG 1692
Db 675 -----AspTrp 676

RESULT 12
US-09-919-497-98
; Sequence 98, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 1736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-98

Alignment Scores:
Pred. No.: 1,736-09 Length: 1736
Score: 220.50 Matches: 135
Percent Similarity: 36.71% Conservative: 108
Best Local Similarity: 20.31% Mismatches: 244
Query Match: 5.35% Indels: 175
DB: 4 Gaps: 28

US-09-502-945-4 (1-2236) x US-09-919-497-98 (1-1736)
QY 358 GTGCGTCTGCAGCGTCTGCACCCGAGCGCTGAGTGTGCTGCTGAG 417
Db 12 ValThrLeuHisArgAlaProGlyPheGlyPheGlyIleAlaIleSerGlyGlyArgAsp 31
QY 418 -----TTTGGCTGTGG-----CTTCTCATCTCCACCTCATCAAGCGGT 459
Db 32 AsnProHisPheGlnSerGlyGluThrSerIleValIleSerAspValLeuLysGlyGly 51
QY 460 CAGGCGACAGCGCTCGGCTCCAGGTAGGGACGAGATCTCGGATCAATGATATCC 519
Db 52 ProAlaGluGly---GlnLeuGlnGluAsnAspArgValAlaMetValAsnGlyValSer 70
QY 520 ATCTCTCTCTGACCATGAGGAGGTCACTCACTTCCG---ACCAAGAAACTGTG 576
Db 71 MetAspAsnValGluHisAlaPheAlaValGlnGlnLeuArgLysSerGlyLysAsnAla 90
QY 577 TCATCAAAAGTACACACATCGGC-----CTGATCCCGTGAAGAGCTCTCTGATGAG 630
Db 91 LysIleThrIleArgArgLysLysValGlnIleProValSerArgProAspProGlu 110
QY 631 CCCTCAGTGGCAGTATGTGGATCATGTTGTGTCGGAATCTGGGGCGCTGGCAGCAGC 690
Db 111 ProValSerAspAsnGluGluAspSerTyrAspGluGluIleHisAspProArgSerGly 130
QY 691 CTGGGCTCCCTGGAAATCGGNAACAAGGAG-----723
Db 131 ArgSerGlyValValAsnArgSerGluLysIleTrpProArgAspArgSerAlaSer 150
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QY 723 -----723
Db 151 ArgGluArgSerLeuSerProArgSerAspArgSerValAlaSerSerGlnProAla 170
QY 724 AAGAAGTCTTTCATCAGCTGCTAGCTCCCA-----GGCCTTGGCTGCACAT 774
Db 171 LysProThrLysValThrLeuValLysSerArgLysAsnGluGluTyrGlyLeuArgLeu 190
QY 775 TCAGCGGCGCCATCCAGAAGCTGTCATCTTTATCAGGCATGTGAAACCTGCTCCCTG 834
Db 191 AlaSer-----HisIlePheValLysGluIleSerGlnAspSerLeu 204
QY 835 TCTGTGAGGTGGGA---TTGGAGATAGGGACAGATTGTGCAATGCTCAATGGCGTCGAC 891
Db 205 AlaAlaArgAspGlyAsnIleGlnGluGlyAspValValLeuLysIleAsnGlyThrVal 224
QY 892 TTCTCTAACCTCGATCACAAGGAGGCTGTAAATGTGCTGCTGAAAAATAGCCGACCTGACC 951
Db 225 ThrGluAsnMetSerLeuThrAspAlaLysThrLeuIleGluArgSerLysGlyLysLeu 244
QY 952 ATCTCCATTGTAGCTGCAGCTGCCGGGAGCTGTTTC-----ATGACAGAC 996
Db 245 LysMetValValGlnArgAspGluArgAlaThrLeuLeuAsnValProAspLeuSerAsp 264
QY 997 CCGGAGCGCTGCGACAGCGCGGCGAGCT-----GAGCTGACGCGGAGGAG 1044
Db 265 SerIleHisSerAlaAsnAlaSerGluArgAspAspIleSerGluIleGln-----281
QY 1045 CTTCTCATGCAAGCGGCTGCGAGTGGAGTCCACACAGATCTCCAGGAGCAGGAGGAG 1104
Db 282 -----SerLeuAlaSerAspHisSerGlyArgSerHisAspArg 294
QY 1105 ATGGAGCGCAAGAGAGAAAGAAATTGCCCAGAGGACAGAGAAATAGAGATAC 1164
Db 295 ProProArgArgSerArgSerProAspGlnArgSerGlnArgSerHisAspHisSer 314
QY 1165 CGNAAGGAGATGGAACAG-----ATTGTAGAGGAGGAAGAAAGTTT 1206
Db 315 ArgHisSerProGlnGlnProSerAsnGlySerLeuArgSerArgAspGluGluArgIle 334
QY 1207 AAGAAGCAATGGAGAGAGACTGGGGCTCAAAGGAACACTACTCTTGCTTAACACATC 1266
Db 335 SerLys-----ProGlyAlaVal 340
QY 1267 ACTGTGTAGGTACACCCAGTACCCCTTCCAAAGCCAAAGATATGATCAGGAGTGAACCT 1326
Db 341 SerThrProValLysHisAlaAspHisThrProLysThrValGluGluVal-----358
QY 1327 GAGCTCGAGCCCGCAGATGACCTGGATGGAGCAGCAGGAGCAGGAGCAGGATTC 1386
Db 359 -----ThrValGluArgAsnGluLysGlnThr 367
QY 1387 CGAAATATGAGGAAGGCTTTGACCCCTACTCTATGTGTTCCACCCAGCAGCAG-----1437
Db 368 ProSerLeuProGluProLysProValTyrAlaGlnValGlyAsnGlnMetTrpIleTyr 387
QY 1438 -----ATCATGGGG 1446
Db 388 LeuSerValHisLeuMetValSerTyrLeuIleGlnLeuMetLysMetGlyPheLeuArg 407
QY 1447 AAGGATGTCGGCTCTACGCATCAAGAAGGAGGATCTTAGACCTGCCCTGGAGGC 1506
Db 408 ProSerMetLysLeuValLysPheArgLysGlyAspSerValGlyLeuArgLeuAlaGly 427
QY 1507 GGTGTGAGTCTCCCATTCGGAAGGTGCTGCTTTCTGCTGTATGAGCGGGAGCTGCT 1566
Db 428 GlyAsnAsp-----ValGly---IlePheValAlaGlyValLeuGluAspSerProAla 444
QY 1567 GAGCGGCATGTGGCATTTGTGAAAGGAGCAGAGATCATGGCAATCAACGCAAGATTGTG 1626
Db 445 AlaLysGlu---GlyLeuGluGluGlyAspGlnIleLeuArgValAsnAsnValAspPhe 463
```

```
QY 1627 ACAGACTACACCTGGCTGAGGCTGAGCTGCCCTGCACAGAGCCCTGGAATCAGGCGGG 1686
Db |||||
464 ThrAsnIleArgGluAlaValLeuPheLeu----- 475
QY 1687 GACTGATCGACTTGTGTTGGCTGCTGCCCTCCAAAGAGGTATGACATGAGCTGACC 1746
Db |||||
476 -----LeuAspLeu-----ProLys-----GlyGluGluValThr 485
QY 1747 TTCCTTGAAGTCCAAAGGGGMAACCAAAATTCAGCGCTTAGGAACACAGTCCGCG 1806
Db |||||
486 IleLeuAlaGlnLysLysLys-----AspValTyr 495
QY 1807 CCCCACTCGTCAACACAAAGCCTCGGACCAAGCTTTGAG-----AGAGCCACATGACACAC 1863
Db |||||
496 ArgArgIleValGluSerAspValGlyAspSerPheTyrIleArgThrHisPheGluTyr 515
QY 1864 ACCAGATGCGATCCTTTGGACCTGAAATCTATCACCCAGGAATCTCAACTCCCTTTGGCC 1923
Db |||||
516 GluLysGluSerProTyrGly-----LeuSer 524
QY 1924 CTGACACCGCCAGATAGGAACAGCTCGGGCCACTTTTGTGAAGGCCAATGTGGAGGA 1983
Db |||||
525 PheAsnLysGlyGluValPheArgAlaValAspThrLeuTyrAsnGlyLysLeu---Gly 543
QY 1984 AAGGGAGCAGCCAGCGCTTTGGGAGAAGATCTCAAGGATCCAGACTCTCATTCCTTTCTCT 2043
Db |||||
544 SerTrpLeuAlaIleArgIleGlyLysAsnHisLysGluValGluArgGlyIleIlePro 563
QY 2044 -----CTGGCCCAAGTGAATTTGGTCTCTCCCA-----GCTTTG 2076
Db |||||
564 AsnLysAsnArgAlaGluGlnLeuAlaSerValGlnTyrThrLeuProLysThrAlaGly 583
QY 2077 GGGGAC 2082
Db |||||
584 GlyAsp 585

RESULT 13
US-09-562-737-24
; Sequence 24, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-24

Alignment Scores:
Pred. No.: 2,83e-09 Length: 724
Score: 215.50 Matches: 110
Percent Similarity: 40.51% Conservative: 82
Best Local Similarity: 23.21% Mismatches: 179
Query Match: 5.23% Indels: 103
DB: 4 Gaps: 21

US-09-502-945-4 (1-2236) x US-09-562-737-24 (1-724)
QY 340 TCCAGGAGCTGAGAGGTGGCTGCGACCGTCTGCACCCCGAGAGCCTCGGCTGAGT 399
Db |||||
155 AlaGluIleIleGluIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 173
QY 400 GTGCGTGGTGGC-----CTGAGATTGGCTGTGGGCTCTTCATCTCCAC 444
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Db |||||
174 TyrAlaGlyGlyValGlyAsnGlnHisIleAlaGlyAspAsnSerIleTyrValThrLys 193
QY |||||
445 CTCATCAAAAGCGGTGAGCA---CACAGCGTCGGCTCCAGTAGGGGACGAGATCGTC 501
Db |||||
194 AspIleGluGlyGlyAlaAlaHisLysAspGluArgLeuGlnIleGlyAspLysIleLeu 213
QY |||||
502 CGGATCAATGGATATTCATCTCCTGTCACCATGAGGCGTTCATCAACCTCATTCGA 561
Db |||||
214 PheValAsnSerValGlyLeuGluAspValGlyHisGluAspAlaValAlaAlaLeuLys 233
QY |||||
562 ---ACCAGAAAACCTGTGCCATCAAGTG-----AGACACATCGGCTGATCCCCGTC 612
Db |||||
234 HisThrTyrAspValValTyrLeuLysValIleLysProSerAsnAlaTyrLeuSerAsp 253
QY |||||
613 AAAAGCTCTCTGTGATGAGCCCTCACT-----TGGCAGTATGTGATCAGTTTGTGTCG 666
Db |||||
254 LysTyrAlaProAspIleThrThrSerLeuSerGlnHisLeuAspAsnGluIleSer 273
QY |||||
666 ----- 666
Db |||||
274 MetSerSerTyrLeuGlyThrAspTyrProAsnAlaMetThrProThrSerProArgArg 293
QY |||||
667 GAATCTGGGGCGCTCGAGGACCTGGCTCCCTCGAAATTCGGGAAAACAGAGAGAG 726
Db |||||
294 GlnSerProValAlaLysAspLeuLeuGly-----ArgGluAspIleProArg 309
QY |||||
727 AAGGCTTCATCAGCTGGTA-----GGCTCCGAGGCTTGGCTGCAGCATTTCCAGC 780
Db |||||
310 GluProArgArgSerValIleHisArgGlySerThrGlyLeuThrPheAsnIleValGly 329
QY |||||
781 GGGCCCATCCAGAACCTGGCATCTTTATCAGCCATGT-----AAACCTGGCTCC 831
Db |||||
330 GlyGlu---AspGlyValGlyIlePheIleSerPheIleLeuAlaTrpGlyProAlaAsp 348
QY |||||
832 CTGCTGCTGAGTGGGATTCGAGATAGGGACACAGATTGTGCGAATTCATCGCTCGAC 891
Db |||||
349 LeuSerGlyGlu-----LeuTyrLysGlyAspGlnIleLeuSerValAsnAlaValAsp 366
QY |||||
892 TTCCTCTAACCTGGATCACAAGGAGGCTGTAATGTGCTGAAAATAAGCCGACCTGACC 951
Db |||||
367 LeuArgAsnAlaSerHisGluAspAlaIleAlaLeuLysAsnAlaGlyGlu---Thr 385
QY |||||
952 ATCTCCATTGTAGCTGCAGCTGGCGGGAGCTGTTTCATGACACAGCGGAGCGCTGGCA 1011
Db |||||
386 ValThrIleIleAlaGln-----TyrLysPheGluGluTyrSerArgPhe 400
QY |||||
1012 GAGCGCGGACGCTGAGCTGCAGCGGACGAGGAGCTT----- 1047
Db |||||
401 GluAlaLysGlyHisAspLeuArgGluGlnLeuMetAsnHisSerLeuGlySerGlyThr 420
QY |||||
1047 ----- 1047
Db |||||
421 AlaSerLeuIleSerAsnProLysArgGlyPheTyrIleLysAlaLeuPheAspTyrAsp 440
QY |||||
1048 -----CTCATGCAAGAGCGCTGGCGATGAGTCCCAACAGATCCTTC 1089
Db |||||
441 LysThrLysLeuCysGlyPheLeuSerGlnAlaLeuSerMetHisPheGlyAspValLeu 460
QY |||||
1090 CAGGAGCAGCAGGAGATGAGCGGCAAGAGGAAAAGAAATTCGCCAGAGACAGCAGAG 1149
Db |||||
461 HisValIleAsnAlaSerAspGluGluTrpTrpGln-----AlaGlnArgValHisSer 478
QY |||||
1150 GAAATGAGAGATACCGGAGGAGATGGACAGATTGTAGAGGAGGAGAGAGTTTAAG 1209
Db |||||
479 AspSerGluThrAspArg-----IleGlyPheIleProSerLysArgSerGluArg 496
QY |||||
1210 AAGCAATGGAA-----GAAGACTGGGCTCA----- 1236
Db |||||
497 ArgGluTrpSerArgLeuLysThrLysAspTrpGlySerSerSerGlySerValGlyArg 516
QY |||||
1237 AAGGAACAGCTACTCTTGCTTAAACCATCACT---GCTGAGGTACAC-----CCA 1284
Db |||||
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Db 517 GluAspSerValLeuSerTyrrTrrThrValThrGlnMetGluValHisTyrrTyrrArgPro 536  
QY 1285 GTACCCCTTGGCAAGCAAGATGATGATCAGGGAGTGGAACTCGAGCTCGAGCCCGCAGAT 1344  
Db 537 IleIleIleLeuGlyProThrAlaAspArgAlaAsnAspLeuSerAspPhePro 556  
QY 1345 GACCTGGATGGAGCAGGAGGAGCAGGAGCAGGATTCGCGAAATATGAGGAGGC 1404  
Db 557 AspLysPheGlySerCysValGluHisThrThrArgProLysArgGluTyrrPheIleAsp 576  
QY 1405 TTGACCCCTACTCTATGTTCCACCCAGCAGCAGATCATGGGAGGAGATGTCGGCTCCTA 1464  
Db 577 GlyArgAspTyrrHisPheValGlySerArgGluLysMetGluLysAspIleHisAlaHis 596  
QY 1465 CGCATCAAGAGGAGGATCTTTAGACCTGGCCCTGGAAGGC 1506  
Db 597 LysPheIleGluAlaGlyGlnIleAsnSerHisLeuTyrrGly 610

RESULT 14  
US-09-252-991A-21827  
; Sequence 21827, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21827  
; LENGTH: 1093  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21827

Alignment Scores:  
Pred. No.: 5,73e-09 Length: 1093  
Score: 219.00 Matches: 212  
Percent Similarity: 33.02% Conservative: 67  
Best Local Similarity: 25.09% Mismatches: 302  
Query Match: 5.29% Indels: 264  
DB: 4 Gaps: 47

US-09-502-945-4 (1-2236) x US-09-252-991A-21827 (1-1093)

QY 2190 AGAGTAAGGTTTGGAGTGAACAATC-----CTGGCAGCAATT 2155  
Db 375 ArgValArgLeuAlaAlaProIleArgArgProProArgLeuSerArgLeuAlaAla 394  
QY 2154 AGAGCAGAGGCGAGA-----GGAGAGGGA 2131  
Db 395 ArgValLysAlaArgSerLeuGluIleSerProProAlaProLeuSerThrAlaProSer 414  
QY 2130 TGGAGAGAGAGACTCCAGTGGGGCTTATTA----- 2098  
Db 415 TrpArgSerSerAlaProGlyValAlaIleArgProProSerArgLeuThrSerVal 434  
QY 2097 -----GGGTTCAAGAGGAGGAGTCCCGCCCAAGCTGG 2068  
Db 435 ProProLeuArgSerArgValThrProValSerLeuThrArgThrProProArgTrrp 454  
QY 2067 GAGAGACCAATTCACTGGGCCAGAGAAAGGAATGAGACTCGGATCTTGAGATCTTC 2008  
Db 455 SerArgProPheArgLeuAlaSerArgProLeuAlaLeu----- 468  
QY 2007 TCCCAACGGCTGGCTGC---TCCCTTCTCCACATTCGCTTCAAAAAGTGGCCGA 1951  
Db 469 -----ThrArgProCysTrpProLeuSerSerArgAlaAla-ThrArgValMetProAl 486

QY 1950 GCTGTTCTTATCTGTGCCCCCTGTGTTACGGGCCAAAGGAGATTGTGAGATTCTCTGGGTGAT-- 1893  
Db 486 aLeuLeuProMetProPro-----LeuArgLeuLeuSerSerTh 499  
QY 1892 -----AGATTACAGTCCCAAGGATGCCATCTGGTGTGTGTCTATGTGGCTCTCTCAAG 1840  
Db 499 rProValArgIleSerThrAlaProLeuAlaIleIleThrProGluArgLeuLeuSerAr 519  
QY 1839 GCTGTGTCGAGGCTTTGTGTTTACAGGAGTGGGGCCGAGCTCACTGTCTTCTAACCGTG 1780  
Db 519 gLeuAlaProCysSerVal---ThrProAlaSerLeuSerLeuProPro----- 535  
QY 1779 AATTGGTTTCCCTTTTGGACTTCAGCAAGAGGTTCAGCTCATCTCATCTACTCTTGTG 1720  
Db 536 ---Trp-----LeuSerSerAlaAlaTrpLeuValSe 545  
QY 1719 GGGGCAGAGCGCAACCAAGGTTCGATCCCGCCCTGATTCCAGGCCCTTCTGCAG 1660  
Db 545 rAlaSerAlaProAlaLeuGluLysVal---ProPro-----ArgLeuSerAr 560  
QY 1659 GGCAGCGTCAGCTTCAGCCAGGGTGTAGTCTGTGTCACAAATCTTGCCGTGTGATGCCATGAT 1600  
Db 560 gArgAlaAlaArgAlaValArgLeuProSerLeuThr----- 572  
QY 1599 CTCGTCCCTTTTCACAATGCCACATGCGCTCAGCAGCTCCCGCTCATACACAGAGA 1540  
Db 573 -----SerAlaProProTrpLeuSerSerThrProProArgLeuThrLeuAr 588  
QY 1539 AACGACCCTTCCCAATGGGGAGTCCACACCGCTTCAGGGCCAGGCTCAAGATCC 1480  
Db 588 gLeuPheTrpLeu-----SerSerArgProProSerProLeuAsnSerSerProPr 605  
QY 1479 CTCCTTCTTTGATGCGTAGGAGCGGACATCTTCCCATGATCTGCTCTGGGGTGAACAT 1420  
Db 605 oSer-----ArgLeuArgProSerArgPro----- 613  
QY 1419 AGAGTAGGGTCAAGGCTTCTCTCATATTTCCGGAATCTGCTCT-----CC 1372  
Db 614 -----AlaSerThrProLeuAlaTrpPheSerArgArgCysThrValArgArgPr 631  
QY 1371 CTGCTCC-----TCGTGCTCCATCCAGGTGATCTGGGGCTCGAGCTCAGGTTCCAC 1318  
Db 631 oLeuSerProMetThrLeuProProArgLeuSerSerCys-SerArgAlaPheThrAlaT 651  
QY 1317 TC-----CCTGATCATATTTGGCTTCGGAAGGGGTACTGGGTG 1279  
Db 651 hrPheGluValLeuGluIleSerProAlaArgLeuSerThrCysArgAlaSerIleAlaM 671  
QY 1278 TACCT-----CAGCAGTGTGTTTATGCAAGAGTAGCTGTCTTCTTGA 1234  
Db 671 etProProPheAlaAlaIleSerGlnAspTrpLeuLeuSerIleVal-----S 687  
QY 1233 GCCCAGCTTCTTCCCATTTGCTTAAACTCTCTTCTCTCTCT-----CTAC 1186  
Db 687 exAlaAlaThrPheArgValPheSerLeuThrSerSerProProCysTrpAlaArgLeuP 707  
QY 1185 AATCTGTTCCA-----TCTCTTCCGGTATCTCTCATTTTCTCTGCTCTCTGGGC 1132  
Db 707 roSerValAlaCysArgSerProLeuAlaAlaIleArgProProAlaLeuProThr----- 725  
QY 1131 AATTTCTTTTCTTTCCTTCCCTCCATCT-----CCTGCTGCTCTGGAGGATCTGTT 1078  
Db 726 -----AlaPheAlaAlaArgSerArgProSerLeuAsnSerLeuProProT 742  
QY 1077 GCACTCCATCGCCAGCGCTTCTGCATGAGAGAGCTCTCCCGCTGAGCTCAGCGTCCG 1018  
Db 742 rpSerLeuArgLeuAlaIleThrSerThrArgThrProAla-LeuProLeuAlaLeuPro 761  
QY 1017 -----CGCTCTGCGAGCGCTCCCGGTCTGTGATGAACAGCTCCCGGCGACGTGAGC 964  
Db 762 ProSerArgLeuSerLysAlaProProValAla-----Leu-LysProAlaSerAl 778

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QY 963 TACAATGGAGATGGTCAGGCTG---CGGCTATTTTTCAGACATTTTACAGCCCTCTCTGTG 907
Db      |||||
QY 778 aThrSerThrProProArgLeuSerArgLeuAlaProTTrpPheAsnSer-----795
Db      |||||
QY 906 ATCCAGGTTAGAGAGTCAGCCATTGACTTCGACAACTCTGGTCCCTATCTCCATCC 847
Db      |||||
QY 796 -LeuArgLeuAspSerArgProProAlaArgLeuSer-----SerCysPr 810
Db      |||||
QY 846 CACCTTCAGCAGCAGGAGCCAGGTTTCATAGGCTGATAAAGATGCCAGGCTTCTGGAT 787
Db      |||||
QY 810 oThrValThrArgCysAlaPro-----TrpLeuSerArgLeuProSer-----824
Db      |||||
QY 786 GGGCCCGCTGGAATCTCGACGCCAAGGCT-----CGGAGCCTACACGGCT 739
Db      |||||
QY 825 -----SerArgLeuSerSerArgProProArgLeuThrSerArgProProArgLe 841
Db      |||||
QY 738 GATGAAGACCTTCTCTCTCTGTTTCCCGATTTCCAGGGAG-----696
Db      |||||
QY 841 uLeuSerValProLeuProLeuLeuSerArgLeuArgAlaArgSerArgArgLeuAl 861
Db      |||||
QY 696 -----696
Db      |||||
QY 861 aAlaGluAsnLysProArgArgLeuSerMetAlaProLeuAlaThrThrSerArgSerSe 881
Db      |||||
QY 695 -----CCCAGGCTGCTCGCAGCCGCCAGATTCGACACAAACTGATC 652
Db      |||||
QY 881 rProLleSerLeuProProArgLeuSerArgLeuPro-----ThrArgAlaSe 897
Db      |||||
QY 651 CACATCTGCCAAGTGAGGGCTCATCAGGAGAGCTTTTCAGGGGATCAGGCCGATGTG 592
Db      |||||
QY 897 rThrArgLeuProGluThrSerProSerProArgLeuThrSerAla-----TrpAl 914
Db      |||||
QY 591 TCTCACTTTGATGGACACAGTTTCTTGGTTCGAATGAGGTTGATGACCTCTCATGGGT 532
Db      |||||
QY 914 aLeuThrArgValAspCysTrpLeuProSerArg-----ProCysTrpPr 929
Db      |||||
QY 531 ACAGGAGGAGATGGAATATCCATTGATCCGAGCATCTCGTCCCTTACCTGGAGCCCGAC 472
Db      |||||
QY 929 oLeuSerSerValAlaAlaProThrThrSerArgSerPheArgProLleThrTrpProProAr 949
Db      |||||
QY 471 GCTGTCTGCTGACCCCTTTTGATG-----AG 445
Db      |||||
QY 949 gLeuSerArgSerProArgValLeuThrThrAlaArgSerArgLeuCysAsnArgProSe 969
Db      |||||
QY 444 GTGGGAGATG-----AAGAGCCACACGCCAACTCCAGGCC 409
Db      |||||
QY 969 rTrpArgLeuSerArgLeuLeuAlaSerThrArgSerSerProSerAlaSerSerLeuPr 989
Db      |||||
QY 408 ACCACGCACACTCAGGCCGAGGCTTCGGGGTGCAGACGGTCCACAGCACCTCTTCAG 349
Db      |||||
QY 989 oProArgLeuSerArg-----CysProProSerThrArgThrValAlaPr 1004
Db      |||||
QY 348 CTTCTGGAGCGCGGGGTGAGCTGATCATATTCACCTGGTGTTCAGTGGGATCAG 289
Db      |||||
QY 1004 oPheArgLeuProProTrpLeuSer-----SerAlaTrpLeuAlaPheAlaSerSe 1021
Db      |||||
QY 288 CGGCCGAATGGCATCAACAGAGGACAGCGGCTGGGTTTCATG-----ATGAC 241
Db      |||||
QY 1021 rAlaArgLeuAlaThr-----ArgLeuProAlaLeuArgValProLeuArg 1037
Db      |||||
QY 240 CAGCTTCAGGCTCTCCACG-----AGCACGGCCACGCTCCATGCT 202
Db      |||||
QY 1037 gSerSerArgSerProArgAlaLeuArgArgSerSerGlySerThrProAlaSer-----1055
Db      |||||
QY 201 CTGGTGATACATTCGACGACATCATAGAGATAGTCTCTCTGCAATATTTTCAATCAG 142
Db      |||||
QY 1056 -----IleThrProAlaLeuSerArgArgAlaAlaSerSerAlaMetArgSerAr 1072
Db      |||||
QY 141 AAATCCACTTATGCGCG---AATTCTCGGCCCACTTTTTCGCTCCATGGCTGGGCCAGG 85
Db      |||||
QY 1072 gAlaAlaArgLeuCysArgLeuThrSerSerSerAlaLeuArgIleSerAlaLeuPro---1091
Db      |||||
QY 84 TCCAGCT 78
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Db      |||||
Db      1092 -ProAla 1093
RESULT 15
US-09-949-016-9739
; Sequence 9739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9739
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9739
Alignment Scores:
Pred. No.: 1,33e-08 Length: 428
Score: 206.00 Matches: 124
Percent Similarity: 37.00% Conservative: 61
Best Local Similarity: 24.80% Mismatches: 184
Query Match: 5.00% Indels: 131
DB: 4 Gaps: 20
US-09-502-945-4 (1-2236) x US-09-949-016-9739 (1-428)
QY 47 GCACCCGAGGAGGAGCGGTCTGCAACG-----ACGCTGAGCCTGCCCGACCA 97
Db      |||||
QY 12 AlaProArgGlySerArgArgProThrValProGlyThrProAlaCysLeuAlaArgPro 31
Db      |||||
QY 98 TGGACCGAAGATGCGCCGAGAAATTCGCGCATPAAAGTGGATTTCTCTGATTGAAATGATG 157
Db      |||||
QY 32 AlaAlaGlnGlyPheSerAlaAlaLeuProValArg-----43
Db      |||||
QY 158 CAGAGAAGACTATCTCTATGATGTGCTGCGGAATGTACCAACAGACCATGAGCGTGGCGG 217
Db      |||||
QY 44 -----TrpThr-GlyAr 47
Db      |||||
QY 218 TGCTCGTGGAGACCTGAAGCTGGTTCATCAATGAACCCAGCCGCTCTGCTCTGTTGTATG 277
Db      |||||
QY 47 gArgAlaGly-----ProSerArgProValProIl 57
Db      |||||
QY 278 CCATTTCG-----GCCGCTGATCCCACTGAAGCACCACGTGGAATATGATGACGTCA 328
Db      |||||
QY 57 eGlyThrProSerArgAlaAlaAspProSerGln-----GlyGluMetSerAlaAs 74
Db      |||||
QY 329 CCCCCCGCGCTCCAGGAGCTGAAGAGGTGCGTCTGGACCGTCTGCACCCCGGAGGCC 388
Db      |||||
QY 74 pAlaAlaAla-GlyAlaProLeuProArgLeuCysCysLeuGluLysGlyProAsnGlyT 94
Db      |||||
QY 389 TCGGCTGAGTGTGCTGGTGGCTGGAGTTTGGC---TGTGGGCTCTTCATCTCCCACC 445
Db      |||||
QY 94 yGlyPheHisLeuHisGly-----GluLysGlyLysLeuGlyGlnTrpIleArgLeuV 112
Db      |||||
QY 446 TCATCAAGAGCGGTTCAGGACAGACGCTCGGCTCCAGGTAGGGGACGAGATCGTCCGGA 505
Db      |||||
QY 112 alGluProGlySerProAlaGluLysAlaGlyLeuLeuAlaGlyAspArgLeuValGluV 132
Db      |||||
QY 506 TCATGGATATTCATCTCTCTCTTACCATGAGAGGTATCAACCTCATCTTCGAAACCA 565
Db      |||||
QY 132 alAsnGlyGluAsnValGluLysGluThrHisGlnGlnValValSerArgIleArgAla- 151
Db      |||||
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Qy	566	AGAAA	CTGTCTCCATCAAACTGAGACACATCGCCGCTGATCCCGTGAAAGCTCTCTCGT	625
Db	152	-----	AlaLeuAsnAlaValArgLeuValValAspProGluThrA	166
Qy	626	ATGAGCC	CTCCTTCAGTATCGGATCAGTTTGTGTCGGA-	669
Db	166	spGluGlnLeu-	GlnLysLeuGlyValGlnValArgLugluLeuLeuArgAlaG	184
Qy	670	-----	-----TCTGGGGCGTTCGAGGCGAGCTGGGCT	697
Db	184	lnGluAlaProGlyGlnAlaGluProAlaAlaAlaGluValGlnGlyAla-	-----	201
Qy	698	CCCCTGGA	AAATCGGGAAAAACAGAGGAAGAAGTCTTCATCAGCCTGGTAGGCTCCCGAG	757
Db	202	-----GlyAsn-	-----GluAsnGluProArgGluAlaAspLysSerHisProGluGlnArgG	219
Qy	758	GCCTTGGC-	-----TGACAGCATTTCCAGCGCCCATC-	789
Db	219	luLeuArgProArgLeuCysThrMetLysLysGlyProSerGlyTyGlyPheAsnLeuH	239	
Qy	790	-----	CAGAAGCCTGGCATCTTTATTCAGCCATGTGAAACCTGGCTCCCTGTCGTG	838
Db	239	isSerAspLysSerLysProGlyGlnPheIleArgSerValAspProAspSerProAlaG	259	
Qy	839	CTGAGTGGG	ATTCGAGATAGGGACACGATTTCTCGAAGTCAATGGCGTGCAGCTTCTCTA	898
Db	259	luAlaSerGlyLeuArgAlaGlnAspArgIleValGluValAsnGlyValCysMetGluG	279	
Qy	899	ACCTGGATCA	CAAGAGGCTGTAAATGTGCTGTAATAATAGCCGAGCCTGCACCATCTCCA	958
Db	279	lyLysGlnHisGlyAspValVal	-----	288
Qy	959	TTGTAGCTGC	AGCTGGCGGGAG-----CTGTTTCATCAGACAGCCGGAGCGGTGGCAG	1012
Db	288	lalieArgAlaGlyGlyAspGluThrLysLeuLeuValValAspArgGlu-	-----	304
Qy	1013	AGCGCGG	CAGCTGAGCTGCAGCGGAGAGCTTCTCATGCAGAAGCGGTGGCGATGG	1072
Db	305	-----	-----ThrAspGluPhePheLysCysArgValIleP	316
Qy	1073	AGTCCAACA	GATCCTCCAG-----GAGCACGAGATGAGC	1111
Db	316	roSerGlnGluHisLeuAsnGlyProLeuProValProPheThrAsnGlyGluIleGlnL	336	
Qy	1112	GGCAAGAGCA	AGAAATTTGCCCAGAGGAGGAGAGAAATAGAGAGA-----T	1162
Db	336	ysGluAsnSerArgGluAlaLeuAlaGluAlaLeuGluSerProArgProAlaLeuV	356	
Qy	1163	ACCGAAGG	AGATGGAAACAGATTTAGAGGAGGAAGAGAGTTTAAAGCAATGGGAAG	1222
Db	356	alArgSerAlaSerSerAspThrSerGluGlu-LeuAsnSerGlnAspSerProProLys	375	
Qy	1223	AAGACTGGG	CTCAAGGAACAGCTACTCTTGCTTAAACCATCATCTGCTGAGGTACACC	1282
Db	376	GlnAspSerThrAlaProSerSerThrSerSerSerAspProIleLeuAspPheAsnIle	395	
Qy	1283	CAGTACCC	CTTCGCAAGCAAGTATGATCAGGAGTGGAACCTGAGCTCGAGCCCGCAG	1342
Db	396	SerLeuAlaMetAlaLysGluArgAlaHisGlnLysArgSerSerLysArgAlaProGln	415	
Qy	1343	ATGACCTGG	ATGGAGCAGGAGGAGCAGGATTTCCGGAATATG	1396
Db	416	MetAspTrp-----	-----SerLysLysAsnGluLeuPheSerAsnLeu	428

Search completed: March 12, 2005, 00:44:01  
Job time : 112.18 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 51.4203 Seconds  
(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-5

Perfect score: 3989

Sequence: 1 cctggccgcgctcgctgc.....tattttccagcttaaaaaa 2162

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2\_1/USPTO\_spool\_p/US09502945/runat 10032005 164737 13306/app query.fasta\_1.10979  
-DB=issued Patents AA -QPMT=fastan -SUFFIX=mar9.rai -MINWATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents AA:\*
- 2: /cgn2\_6/ptodata/1/iaa/5A COMB pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/5B COMB pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6A COMB pep:\*
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- 6: /cgn2\_6/ptodata/1/iaa/6CTUS COMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273	6.8	2046	4	US-09-949-016-9365
2	263	6.6	2037	4	US-09-306-998-3
3	250.5	6.3	1881	3	US-09-233-086-3
4	234.5	5.9	767	4	US-09-317-254-69
5	234.5	5.9	767	4	US-09-919-497-59
6	232.5	5.8	533	4	US-09-270-767-42903
7	232	5.8	1771	4	US-09-949-016-9470
8	229.5	5.8	724	4	US-09-562-737-21
9	225	5.6	1736	4	US-09-919-497-98
10	211	5.3	724	4	US-09-562-737-28
11	210.5	5.3	724	4	US-09-562-737-23
12	206.5	5.2	1050	3	US-09-045-632-50

13	204.5	5.1	2466	3	US-09-080-855-12	Sequence 12, Appl
14	204.5	5.1	2466	4	US-09-566-076-12	Sequence 12, Appl
15	204.5	5.1	2466	5	PCT-US94-09943-2	Sequence 2, Appl
16	204.5	5.1	2485	3	US-09-290-640-46	Sequence 46, Appl
17	204.5	5.1	2485	4	US-09-665-615B-46	Sequence 46, Appl
18	203.5	5.1	1050	3	US-09-045-632-49	Sequence 49, Appl
19	202	5.1	1112	3	US-09-045-632-2	Sequence 2, Appl
20	202	5.1	1112	3	US-09-045-632-3	Sequence 3, Appl
21	201	5.0	604	3	US-09-045-632-14	Sequence 14, Appl
22	201	5.0	702	3	US-09-045-632-15	Sequence 15, Appl
23	201	5.0	1018	3	US-09-045-632-16	Sequence 16, Appl
24	201	5.0	1061	3	US-09-045-632-32	Sequence 32, Appl
25	199	5.0	724	4	US-09-562-737-22	Sequence 22, Appl
26	199	5.0	2465	2	US-08-596-291-3	Sequence 3, Appl
27	199	5.0	2465	3	US-09-100-804-3	Sequence 3, Appl
28	193	4.9	724	4	US-09-562-737-30	Sequence 30, Appl
29	193	4.9	450	2	US-08-665-037-2	Sequence 2, Appl
30	193.5	4.9	450	2	US-08-666-067-2	Sequence 2, Appl
31	193.5	4.9	450	2	US-08-732-870-2	Sequence 2, Appl
32	192.5	4.8	428	4	US-09-949-016-9719	Sequence 9739, Ap
33	192	4.9	663	4	US-09-252-991A-30843	Sequence 30843, A
34	191.5	4.8	131	4	US-09-270-767-33426	Sequence 33426, A
35	191.5	4.8	131	4	US-09-270-767-48643	Sequence 48643, A
36	191.5	4.8	534	4	US-09-949-016-8945	Sequence 8945, Ap
37	190	4.8	724	4	US-09-562-737-26	Sequence 26, Appl
38	188.5	4.7	724	4	US-09-562-737-24	Sequence 24, Appl
39	188.5	4.7	836	4	US-09-252-991A-26065	Sequence 26065, A
40	188	4.7	1093	4	US-09-252-991A-21827	Sequence 21827, A
41	186.5	4.7	724	4	US-09-562-737-29	Sequence 29, Appl
42	186	4.7	507	3	US-09-045-632-13	Sequence 13, Appl
43	185	4.6	774	4	US-09-252-991A-16789	Sequence 16789, A
44	185	4.6	917	4	US-09-252-991A-25101	Sequence 25101, A
45	184	4.6	358	4	US-09-740-027-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-9365  
; Sequence 9365, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9365  
; LENGTH: 2046  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9365

Alignment Scores:			
Pred. No.:	1.05e-14	Length:	2046
Score:	273.00	Matches:	146
Percent Similarity:	36.78%	Conservative:	71
Best Local Similarity:	24.75%	Mismatches:	170
Query Match:	6.84%	Indels:	203
DB:	4	Gaps:	25

US-09-502-945-5 (1-2162) x US-09-949-016-9365 (1-2046)

QY 11 TCOCGCTCGCGCTCTTTTCCAGCTCTCTGCGAGCCGCCGAA-----GGAAACG 61



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DB 1552 SerGlnSerLeuMetValProGlnSerGlySerProGluProGluSerLeuArgAsnThr 1571
QY 62 GGTGTCGAACGACGAGCTGGACCTGGCCAGCCATGGACCGAAGAGTGGCCGAGAAAT 121
DB 1572 SerArgSerSerThrProAlaIlePheAla-Ser---AspProAlaThrCysProIleI 1590
QY 122 TCCGGCATAGGTTCTGATTTGAAATGATGC----- 158
DB 1590 eProGly-----CysGluThrThrIleGluIleSerLy 1601
QY 159 ----AGAGAAGGACTATCTATGATGTGCTG----- 186
DB 1601 sGlyArgThrGlyLeuGlyLeu-SerIleValGlyGlySerAspThrLeuLeuGlyAlaI 1621
QY 187 -----CGAATGTATCCACCAG-----ACCATGGACGTGGCGCTGCTCGTG 226
DB 1621 leIleIleHisGluValTyrgluGluGlyAlaAlaCysLysAspGlyArgLeuTipAlaG 1641
QY 227 GAGACCTGAAGCTGGTCATCAAT----- 249
DB 1641 lyAspGlnIleLeuGluValAlaAsnGlyIleAspLeuArgLysAlaThrHisAspGluAlaI 1661
QY 250 -----GAACCCAGCGCTCTGCTCTGCTGTGATGATCCATTCGSCCGCTGA 292
DB 1661 leAsnValLeuArgGlnThrProGlnArgValArgLeu---ThrLeuTyrgAspGluA 1680
QY 293 TCCCACTGAAGCACAGGTGGAAATATGATCAGCTGACCCCGCGCGCTCCAGGAAGCTGA 352
DB 1680 laProTyrgLysGluGluGluValCysAspThrLeuThr----- 1692
QY 353 AGAGAGTGGCTTGGACCGTCTGCACCCGAGAGCGCTCGCGCTGAGTGGCGTGGCGC 412
DB 1693 ----IleGluLeuGlnLysLysProGlyLysGlyLeuGlyLeuGlyIleValGlyLysA 1711
QY 413 TGGAGTTTGGCTGTGGGCTTCTCATCTCCACCTCATCAAGCGCTCAGGACAGCAGC 472
DB 1711 rgAsn---AspThrGlyValPheValSerAspIleValLysGlyIleAlaAspAlaA 1730
QY 473 TCGGG---CTCCAGGTAGGGGACGATCGTCCGGATCAATGATGATTCATCTCCTCCT 529
DB 1730 spGlyArgLeuMetGlnGlyAspGlnIleLeuMetValAsnGlyGluAspValArgAsnA 1750
QY 530 GTACCATGAGGAGGTATCACTCATTCGA---ACCAAGAAAACCTGTGTCCATCAAG 586
DB 1750 laThrGlnGluAlaValAlaAlaLeuLeuLysCysSerLeuGlyThrValThrLeuGluV 1770
QY 587 TGAGACATCGCGCTGATCCCGTGAAGCTCT-----CCTGATGAG----- 630
DB 1770 aIGlyArgIleLysAlaGlyProPheHisSerGluArgProSerGlnSerSerGlnV 1790
QY 631 -----CCCTCACTTGGCAGTATGTGATCACT 658
DB 1790 aISerGluGlySerLeuSerSerPheThrPheProLeuSerGlySerSerThrSerGluS 1810
QY 659 TTGTGTCGAATCTGGGGCGTCGAGCAGCGCTGGGCTCC-----CCTGGAATCGGG 712
DB 1810 erLeu---GluSerSerSerLysLysAsnAlaLeuAlaSerGluIleGlnGlyLeuArgT 1829
QY 713 AAAACAAGGAGAGAGGTCTTCATCAGCTGTGAGCTCCCGAGCGCTTGGTCGAGCA 772
DB 1829 hrValGluMetLysLys-----GlyProThrAspSerLeuGlyIleSerI 1844
QY 773 TTTCAGCGCGC-----CCCATCCAGAAGCGCTGTCATCTTTATCAGCCATCGAAAC 823
DB 1844 leAlaGlyValGlySerProLeuGlyAspValProIlePheIleAlaMetMetHisP 1864
QY 824 CTGGCTCCCTGCTCTGAGGTG---GGATTGGAGATAGGGACCAAGATTGTGCAAGTCA 880
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## RESULT 3

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US-09-233-086-3
; Sequence 3, Application US/09233086
; Patent No. 6337192
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC1 Gene
; CURRENT APPLICATION NUMBER: US/09/233,086
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: US 60/071,861
; EARLIER FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1881
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QY 881 ATGCGGCTCGACTTCTTAACCTGGATCAAGAGGCTGTAAATGTGCTGAAATAAGCC 940
DB 1884 ysGlyThrSerThrGluGlyMetThrHisThrGlnAlaValaAsnLeuLeuLysAsnAla- 1903
QY 941 GGAGCTGACCATCTCCATTTAGCTGAGCTGGCCGGAGCTGTTTCATGACAGACGGG 1000
DB 1904 --SerGlySerIleGluMetGlnValAlaGly-GlyAspValSerValValThrGly 1922
QY 1001 AGCGGCTGCAGAGCGCGCGAGCTGAGCTGCAGCGCGAGGAGCTTCTCATCAGAAGC 1060
DB 1922 ----- 1922
QY 1061 GGCTGGCGATGGATGCCAACAAAGATCTCCAGGAGCAGCAGAGATACCGGAAGGAGTGAAC 1120
DB 1922 ----- 1922
QY 1121 GAAAGAAATTTGCCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1180
DB 1922 ----- 1922
QY 1181 AGATTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1240
DB 1922 ----- 1922
QY 1241 AACAGCTACTTTCCTAAACCATCACTGCTGAGGTACACCCAGTACCCCTTTCGCAAGC 1300
DB 1923 -----HisGlnGlnGluProAlaSerSer 1930
QY 1301 CAAAGTGATTTCCGGAATATGAGGAAGGCTTTGACCCCTACTCTATGTTTACCC----- 1354
DB 1931 SerLeuSerPhe-----ThrGlyLeuThrSerSerSerIlePheGlnAspAsp 1946
QY 1355 -----CCAGACAGATCATGGGAGGAGGATTCGGCTCTCAGCATCAAGAGGAGGAGG 1408
DB 1947 LeuGlyProProGlnCys-----LysSerIleThrLeuGluArg-----GlyProAsp 1962
QY 1409 TCTTAGACTCGCCCTCGAAGCGGTGGAGCTCCCGCATTTGGG-----AAGGTGGTC 1462
DB 1963 GlyLeuGlyPheSerIleValGlyTyrgLysSerProHisGlyAspLeuProIleTy 1982
QY 1463 GTTCTGCTGTATGAGCGGGAGCTGCTAGCGGCGATGTTGGCATTTGTGAAAGGGGAC 1522
DB 1983 ValLysThrValPheAlaLysGlyAlaAlaSerGluAspGlyArgLeuLysArgGlyAsp 2002
QY 1523 GAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTGCTGAGGCTGAGCTG 1582
DB 2003 GlnIleIleAlaValaAsnGlyGlnSerLeuGluGlyValThrHisGluGluAlaValAla 2022
QY 1583 GCCTGCGAGAAG 1594
DB 2023 IleLeuLysArg 2026
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		; ORGANISM: Homo sapiens			
		US-09-233-086-3			
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Score:		250.50	Matches:	155	
Percent Similarity:		36.03%	Conservative:	117	
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Query Match:		6.28%	Indels:	202	
DB:		3	Gaps:	28	
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QY	70	AAACGACGAGCTGGAGCTGGCCGACCATGGACCGAAGTGGCCGAGATTCGGGCAT	129		
DB	991	AsnAspValGlnGlyProSerLeuLeuIleAspLeuProValAlaGlnArgArgGlu	1010		
QY	130	AAGGTGGATTTCTGATTGAAATGATGACAGAGGACTATCTCTATGATGTGCTCGGA	189		
DB	1011	GlnGluAsp-----	LeuPro 1015		
QY	190	ATGTAC---CACAGACCATGAGCTGGCCGCTGCTGCTGGGAGACTGAAGCTGTCATC	246		
DB	1016	LeuTyrGlnHisGlnAla-----	ThrArgValIle 1025		
QY	247	AATGAACCCAGCGCTGCTGCTCTGTTTGATGCCATTTCGGCCGCTGATCCCACTGAAGCAC	306		
DB	1026	SerLysAlaSer-----	AlaTyrThrGlyMetLeuSerSerArgTyr 1039		
QY	307	CAGGTGGAAATATATGATGATGACCCCGCGCTCCAGAAAGCTGAAGGAG-----	357		
DB	1040	AlaThrAspThrCysGlnLeuProGluArgGluGluGlyGluGlyGluGluThrProAsn	1059		
QY	358	-----GTGCGTCTGGACCGCTCTGCACCCCGAAGGCCCTC	390		
DB	1060	PheSerHisTrpGlyProProArgIleValGluIlePheArgGluProAsnValSerLeu	1079		
QY	391	GGCTCAGTGTGGTGGTGGC-----CTGGAGTTTGGC-----	423		
DB	1080	GlyIleSerIleValGlyGlnThrValIleLysArgLeuLysAsnGlyGluGluLeu	1099		
QY	424	TGTGGCTCTTCATCTCCACCTCATAAAGCGGTGAGGACAGACAGCGTC---GGGCTC	480		
DB	1100	LysGlyIlePheIleLysGlnValLeuGluAspSerProAlaGlyLysThrAsnAlaLeu	1119		
QY	481	CAGGTAGGGAGCAGATCTCGGATCAATGGATATTCATCTCTCTGTACCATGAG	540		
DB	1120	LysThrGlyAspLysIleLeuGluValSerGlyValAspLeuGlnAsnAlaSerHisSer	1139		
QY	541	GAGGTCACTCACTCATTCGAACCAAG---AAAACGTGTCTCATCAAGTGAACACATC	597		
DB	1140	GluAlaValGluAlaIleLysAsnAlaGlyAsnProValValPheIleValGlnSerLeu	1159		
QY	598	GGC-----CTGATCCCGCTGAAAGCTCTCTGTATGAGCCCTCACTTGGCGAG	645		
DB	1160	SerSerThrProArgValIleProAsnValHisAsnLysAlaAsnLysIleThr---Ser	1178		
QY	646	TATGTGGATCAGTTGTGCGAATCTGGGGCGGTGCGAGGACGCTGGGCTCCCTCT---	702		
DB	1179	AsnGlnAsnGlnAspThrGlnGluLysLysGluLysArgGlnGlyThrAlaProPro	1198		
QY	703	-----GGAATCGGAAACCAAGGAGAG	726		
DB	1199	MetLysLeuProProTyrLysAlaLeuThrAspAspSerAspGluAsnGluGlu	1218		
QY	727	AAGGTCTTC-----ATCAGCTGTGTAGGC-----	750		
DB	1219	AspAlaPheThrAspGlnLysIleArgGlnArgTyrAlaAspLeuProGlyGluLeuHis	1238		
QY	751	-----TCCCGAGGCTTGGCTGCGAGCATTTCCAGCGGCCCCCATC	789		
DB	1239	IleIleGluLeuGluLysAspLysAsnGlyLeuGlyLeuSerLeuAlaGlyAsnLysAsp	1258		



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QY 1537 CAACGCGAAGATTGTGACAGACTACACCCCTGGCTGAGGCTGAGCTGCGCTCGCAGAGGC 1596
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Db 618 eAspGlyArg-----AspYrHisPheValSerSerArgGluLysMetGluLys-- 634
QY 1597 CTGGAATCAGGGCGGGGACTGGATCGACCTTGTGTTGCTGCTGCGCCCAAGAGGATG 1656
634 ----- 634
QY 1657 TGACGATGAGTGACCTTCTGCTGAAGTCCAAAGGGGAAACCAAAATTCACGCGTTAGG 1716
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Db 635 -AspIleGlnAlaHisLysPheIleGluAlaGlyGlnTyrAsnSer---HisLeuTyrGln 653
QY 1717 AAACAGT-----GAGCTCCGGCCCACTCGTGAACACACAA 1752
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Db 653 YThrSerValGlnSerValArgGluValAlaGluGlnGlyLysHisCysIleLeuAspVa 673
QY 1753 GCCTCGGACCGCTTGAGAGAGGCCACATGACACACAGATGGCATCTTGGGACCT 1812
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 673 lSerAlaAsnAlaValArgArgLeuGlnAlaHisLeu-----HisProIleAlaI 691
QY 1813 GAATCTATCACCAGGAATCTCAACTCCCTTTGGCCCTGAAC----- 1855
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 691 ePheIleArgProArgSerLeuGluAsnValLeuGluIleAsnLysArgIleThrGluGln 711
QY 1856 -CAGGSCCAGATAAGGAACAGCTCGGGCCACTTTTGAAG----- 1895
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 711 uGln-AlaArgLysAlaPheAspArgAlaThrLysLeuGluGlnGluPheThrGluCysP 731
QY 1896 -----GCCAATGTGGAGGAAGGAGCAGCCAGCCGCTTTGGGAGAGATCTCAAGG---A 1947
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 731 heSerAlaIleValGluGlyAspSerPheGluGluIleTyrHisLysValLysArgValI 751
QY 1948 TCCAGACTCTCATT---CCTTCTCTCTGG 1973
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Db 751 leGluAspLeuSerGlyProTyrIleTrp 760

RESULT 5
US-09-919-497-59
; Sequence 59, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Muttler, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-59

Alignment Scores:
Pred. No.: 1,4e-11 Length: 767
Score: 234.50 Matches: 144
Percent Similarity: 38.10% Conservative: 104
Best Local Similarity: 22.12% Mismatches: 210
Query Match: 5.88% Indels: 193
DB: 4 Gaps: 34

US-09-502-945-5 (1-2162) x US-09-919-497-59 (1-767)
QY 340 TCCAGGAAGCTGAAGAGGTGGCTCTGGACCGTCTGCACCCGGAAGGCTCGGCTCGAGT 399
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 198 AlaGluLysValMetGluIleLysLeuLysLysLysLysLysLysLysLysLysLysLys 216
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QY 400 GTGCGTGTGGC-----CTGGAGTTTGGCTGTGGCTCTTCATCTCCAC 444
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Db 217 lLeAlaGlyValGlyAsnGlnHisIleProGlyAspAsnSerIleTyrValThrLys 236
QY 445 CTCATCAAGCGGTGACGACACACCGTCGGG---CTCCAGGTAGGGGACGAGATCGTC 501
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 237 lIleIleGluGlyGlyAlaAlaHisLysAspGlyArgLeuGlnIleGlyAspLysIleLeu 256
QY 502 CGGATCAATGGATATTCCTCTCTCTGATCCCATGAGGAGGTGCATCAACCTCATTCGA 561
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 257 AlaValAsnSerValGlyLeuGluAspValMetHisGluAspAlaValAlaLeuLys 276
QY 562 ---ACCAAGAAATGTGTCCATCAAGTG-----A3ACATCGCGCTGTATCCCC 609
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 277 AsnThrTyrAspValValTyrLeuLysValAlaLysProSerAsnAlaTyrLeuSerAsp 296
QY 610 GTGAAAGCTCTCTGATGATGCGCCCTCACTGG---CAGTATGTGTGATCAGTTTGTGTCG 666
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 297 SerTyrAlaProProAspIleThrThrSerTyrSerGlnHsLeuAspAsnGluIleSer 316
QY 667 GAATCTGGGCGCTCGAGGAGCGCTGGC----- 696
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 317 HisSer-----SerTyrLeuGlyThrAspTyrProThrAlaMetThrProThr 332
QY 697 -----TCCCTCGAAATCGGAA-----AACAG 720
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 333 SerProArgArgTyrSerProValAlaLysAspLeuLeuGlyGluGluAspIleProArg 352
QY 721 CAGAAAGAGGTCTTCATCAGCTGTAGGCTCCCGAGGCTTGGCTGCAGCATTTCCACG 780
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 353 GluProArgArgIleValIleHisArgGlySerThrGlyLeuGlyPheAsnIleValGly 372
QY 781 GCGCCCATCCAGAACCTCGGCATCTTTTATCAGCCATGTG-----AAACCTGGCTCC 831
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 373 GlyGlu---AspGlyGluGlyIlePheIleSerPheIleLeuAlaGlyGlyProAlaAsp 391
QY 832 CTGTCTGTGAGGTGGGATTTGGAGATAGGGACAGATTTGTGAAGTCAATCGGCTGCAC 891
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 392 LeuSerGlyGlu-----LeuArgLysGlyAspGlnIleLeuSerValAsnGlyValAsp 409
QY 892 TTCTCTAACCTGGATCACAAGGAGGCTGTAAATGTGCTGAAATAATAGCGCAGCTGACC 951
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 410 LeuArgAsnAlaSerHisGluGlnAlaAlaIleAlaLeuLysAsnAla---GlyGlnThr 428
QY 952 ATCTCCATTTAGTGCAGCTGCGCGGAGCTGTTTCATGACACAGCCGAGGCGGCTGGCA 1011
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 429 ValThrIleIleAlaGln-----TyrLysProGluGluTyrSerArgPhe 443
QY 1012 GAGCGCGGACGCTGAGCTGCAGCGGAGGAGCTTCTCATTCAGAGCGGCTGGGATG 1071
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 444 GluAlaLysIleHisAspLeuArgGluGln-----LeuMetAsnSerSerLeuGlySer 461
QY 1072 GAGTCCAACAGATCTCTCCAGGAGCAGCAGGAG-----ATGGAG 1110
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 462 GlyThrAlaSerLeuArgSerAsnProLysArgGlyPheTyrIleArgAlaLeuPheAsp 481
QY 1111 CGGCAAGAGGAGAAAGAAATTCGCCAGAGGAGCAGAGAGGAGGAGGAGGAGGAGGAG 1170
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 482 TyrAspLysThrLysAspCysGlyPheLeuSerGlnAlaLeuSerPheArgPheGlyAsp 501
QY 1171 GAGATGGAAACAGATTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1206
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 502 ValLeuHisValIleAspAlaSerAspGluGluTyrTrpGlnAlaArgValHisSer 521
QY 1207 -----AAGAGCAA 1215
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 522 AspSerGluThrAspAspIleGlyPheIleProSerLysArgArgValGluArgGlu 541
QY 1216 TGGGAA-----GAAGACTGGGCTCA-----AAGGAA 1242
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 542 TrpSerArgLeuLysAlaLysAspTrpGlySerSerSerGlySerGlnGlyArgGluAsp 561
QY 1243 CAGCTACTCTTCCTGCTAAACCATCACT---GCTAGGTACACCCAGTACCCCTTCGCAAG 1299
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 562 SerValLeuSerTyrGluThrValThrGlnMetGluValHisIleTyrAlaArg----- 578
```





```

; ; ; ; ;
456 AspAlaGlnGlnProThrGlyProSerValLeuAlaAlaAlaMetValHisGly 475
; ; ; ; ;
1240 GAACAGCTACTCTTGCCTAAACCATCATCTGCTAGGTACACCCAGTACCCCTTCCCAAG 1299
; ; ; ; ;
476 AlaSerSerProThrProProAlaAlaThrSerAsnIleThrProLeuProThrAlaAla 495
; ; ; ; ;
1300 CCA 1302
; ; ; ; ;
496 Pro 496

RESULT 7
US-09-949-016-9470
; Sequence 9470, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9470
; LENGTH: 1771
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9470

Alignment Scores:
Pred. No.: 3-73e-11 Length: 1771
Score: 232.00 Matches: 144
Percent Similarity: 38.63% Conservative: 116
Best Local Similarity: 21.40% Mismatches: 236
Query Match: 5.82% Indels: 177
DB: 4 Gaps: 31

US-09-502-945-5 (1-2162) x US-09-949-016-9470 (1-1771)
QY 310 GTGGAATATGATCAGTACCCCGG-----CGCTCCAGGAAGCTGAAGGAG 357
; ; ; ; ;
D 19 LeuGluArgAspLysMetSerAlaArgAlaAlaAlaLysSerThrAlaMetGluGlu 38
; ; ; ; ;
QY 358 -----GTGCGTCTGGACCGCTGCACCCCGAAGCCTCGGC 393
; ; ; ; ;
D 39 ThrAlaIleTrpGluGlnHisThrValThrLeuHisArgAlaProGlyPheGly 58
; ; ; ; ;
QY 394 CTGAGTGTGCGTGGCGCTGAG-----TTGGCTGTGGG-----CTCTTC 435
; ; ; ; ;
D 59 IleAlaIleSerGlyGlyArgAspAsnProHisPheGlnSerGlyGluThrSerIleVal 78
; ; ; ; ;
QY 436 ATCTCCCACTCATCAAGCGGTCCAGGACAGCGTCCGGCTCCAGTGAAGGACGAG 495
; ; ; ; ;
D 79 IleSerAspValLeuLysGlyGlyProAlaGluGly---GlnLeuGlnGluAsnAspArg 97
; ; ; ; ;
QY 496 ATCTGTCGGATCAATGGATATTCATCTCTCTGTACCCATGAGGAGTCAACCTC 555
; ; ; ; ;
D 98 ValAlaMetValAsnGlyValSerMetAspAsnValGluHisAlaPheAlaValGlnGln 117
; ; ; ; ;
QY 556 ATTCTGA---ACCAAGAAACTGTGTCCATCAAGTACAGACACATCCG-----CTGATC 606
; ; ; ; ;
D 118 LeuArgLysSerGlyLysAsnAlaLysIleThrIleArgArgLysLysValGlnIle 137
; ; ; ; ;
QY 607 CCGGTGAAGTCTCTCTGATGAGCCCTCACTTGGCAGTATGTGATCAGTTTGTGCG 666
; ; ; ; ;
D 138 ProValSerArgProAspProGluProValSerAspAsnGluAspSerTyrAspGlu 157
; ; ; ; ;
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QY 667 GAATCTGGGGCGTGCAGGACGCGCTGCGCTCCCTCGAAATCGGAAACCAAGCAG--- 723
; ; ; ; ;
D 158 GluIleHisAspProArgSerGlyArgSerGlyValValAsnArgArgSerGluLysIle 177
; ; ; ; ;
QY 723 ----- 723
; ; ; ; ;
D 178 TrpProArgAspArgSerAlaSerArgGluArgSerLeuSerProArgSerAspArgArg 197
; ; ; ; ;
QY 724 -----NAGAAGTCTTCATCA3CCTGGTAGGCTCCCGA--- 756
; ; ; ; ;
D 198 SerValAlaSerSerGlnProAlaLysProThrLysValThrLeuValLysSerArgLys 217
; ; ; ; ;
QY 757 -----GGCCTTGGCTGCAGCATTTCCAGCGCCCATCCAGAAGCCTGGCATCTTTATC 810
; ; ; ; ;
D 218 AsnGluGluTyrGlyLeuArgLeuAlaSer-----HisIlePheVal 231
; ; ; ; ;
QY 811 AGCCATGTGAACCTGGCTCCCTGTCTGTAGGTGGGA---TTGGAGATAGGGACCAAG 867
; ; ; ; ;
D 232 LysGluIleSerGlnAspSerLeuAlaAlaArgAspGlyAunIleGlnGluGlyAspVal 251
; ; ; ; ;
QY 868 ATTGTGGAAGTCAATGGCGTGCAGTCTTCAACCTGGATCAACAGGAGCTGTAAATGTG 927
; ; ; ; ;
D 252 ValLeuLysIleAsnGlyThrValThrGluAsnMetSerLeuThrAspAlaLysThrLeu 271
; ; ; ; ;
QY 928 CTGAAAAATAGCGCAGCGCTGACCATCTCCATTGTAGCTGCAGCTGCCCGGAGCTGTT 987
; ; ; ; ;
D 272 IleGluArgSerLysGlyLysLeuLysMetValValGlnArgAspGluArgAlaThrLeu 291
; ; ; ; ;
QY 988 ATG-----ACAGCCGGGAGCGG 1005
; ; ; ; ;
D 292 LeuAsnValProAspLeuSerAspSerIleHisSerAlaAsnAlaSerGluArgAspAsp 311
; ; ; ; ;
QY 1006 CTGGCAGAG----- 1014
; ; ; ; ;
D 312 IleSerGluIleGlnSerLeuAlaSerAspHisSerGlyArgSerHisAspArgProPro 331
; ; ; ; ;
QY 1015 -----GCGCGGCGAGCGTGAGCTG---CAGCGGCGAGGAGCTTCTCATGCAGAAAGCGGCTG 1065
; ; ; ; ;
D 332 ArgArgSerArgSerArgSerProAspGlnArgSerGluProSerAspHisSerArgHis 351
; ; ; ; ;
QY 1066 GCGATGGAG-----TCCAACAAGATCTCCAGGAGCAGCAAGAGATGAGCGGCAAGG 1119
; ; ; ; ;
D 352 SerProGlnGlnProSerAsnGlySerLeuArgSerArgAspGluGluArgIleSerLys 371
; ; ; ; ;
QY 1120 AGAAAGAAATGCCCCAGACGACAGGAAATAGAGATACCGGAGAGAGATGGAA 1179
; ; ; ; ;
D 372 ProGlyAlaValSerThrProValLysHisAlaAspAspHisThrProLysThrValGlu 391
; ; ; ; ;
QY 1180 CAGATT---GTAGAGGAGAGAGAGAAAGTTTAAGAAGCAATGCGAAGAGACTGGGGCTCA 1236
; ; ; ; ;
D 392 GluValThrValGluArgAsnGluLysGlnThrProSerLeuProGlu----- 407
; ; ; ; ;
QY 1237 AAGGAACAGCTACTCTTGCCTAAAAACCATCATCTGCTGAGGTACACCCAGTACCCCTCGC 1296
; ; ; ; ;
D 408 -----ProLysProValTyrAlaGlnValGlyGln----- 417
; ; ; ; ;
QY 1297 AAGCCAAAGTATTTCGGAATATAGAGAGGCTTTGACCCCTACTCTATGTTTACCCCC 1356
; ; ; ; ;
D 418 -----ProAspValAspLeuProValSerProSerAspGlyValLeuPro 432
; ; ; ; ;
QY 1357 AGAGCAGATCATGCGGAAGGATGTC-----CGCTCTCTACGCATCAAGAA 1401
; ; ; ; ;
D 433 AsnSerThrHisGluAspGly-IleLeuArgProSerMetLysLeuValLysPheArgLys 452
; ; ; ; ;
QY 1402 GGAGGATCTTTAGACCTGGCCCTCGAAGCGGCTGGAGCTCCCATTTGGGAAGGTGT 1461
; ; ; ; ;
D 452 sclyAspSerValGlyLeuArgLeuAlaGlyGlyAsnAsp-----ValGly---IlePhe 469
; ; ; ; ;
QY 1462 CGTTTCTCTGTATGATGAGCGGAGCTGCTGAGCGGAGTGGTGGCATTGTGAAAGGGA 1521
; ; ; ; ;
D 469 eValAlaGlyValLeuGluAspSerProAlaAlaLysGlu---GlyLeuGluGluGlyAs 488
; ; ; ; ;
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QY 1522 CGAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTCGCTGAGGCTGACGC 1581
Db pGinIleLeuArgValAsnAsnValAspPheThrAsnIleIleArgGluGluAlaValLe 508
QY 1582 TGCCCTGCAGAGGCTTGAATCAGGCGGGACTGATCGACTTGTGTGCTGCTGCTG 1641
Db uPheLeu-----LeuAspLeu----- 513
QY 1642 CCCCCCAAGAGTATGACAGTACGCTGACCTTCTTCTGTAAGTCCAAAAGGGGAAACCA 1701
Db -----ProLys-----GlyGluGluValThrIleLeuAlaGlnLysLys----- 527
QY 1702 AATTCAGCGTTAGGAACAGTACGCTCGGCCCCACCTCGTGAACACAAAGCCTCGGAC 1761
Db -----AspValTyrArgArgIleValGluSerAspValGlyAs 540
QY 1762 CAGCCTTGAG---AGAGGCCACATGACACACACAGATGCGATCCTTGGGACCTGAATCT 1818
Db pSerPheTyrIleArgThrHisPheGluTyrGluLysGluSerProTyrGly----- 557
QY 1819 ATCACCAGGAATCTCAAACTCCCTTTGGCCCTTGAACACGAGCCAGATGAAGAACACGCTC 1878
Db -----LeuSerPheAsnLysGlyGluValPheArgValVa 569
QY 1879 GGGCCACTTTTGAAGGCCAATGTGAGGAAGGGAGCAGCCGCTTTGGGAGAAGA 1938
Db lAspThrLeuTyrAsnGlyLysLeu---GlySerTrpLeuAlaIleArgIleGlyLysAs 588
QY 1939 TCTCAAGGATCCAGACTCTCATCTCTTCTCT-----CTGGCCCCA 1977
Db nHisLysGluValGluArgGlyIleIleProAsnLysAsnArgAlaGluGlnLeuAlaSe 608
QY 1978 GTGAATTTGGTCTCTCCCA-----GCTTTGGGGGAC 2008
Db rValGlnTyrThrLeuProLysThrAlaGlyGlyAsp 620

RESULT 8
US-09-562-737-21
; Sequence 21, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-21

Alignment Scores:
Pred. No.: 3,7e-11 Length: 724
Score: 229.50 Matches: 146
Percent Similarity: 37.54% Conservative: 101
Best Local Similarity: 22.19% Mismatches: 204
Query Match: 5.75% Indels: 207
DB: 4 Gaps: 35

US-09-502-945-5 (1-2162) x US-09-562-737-21 (1-724)
QY 340 TCAGGAAGCTGAAGAGGTGCTCTGGAGCCGCTGCACCCCGAAGGCTCGGCTGAGT 399
Db -----GlyProLysGlyLeuGlyPheSer 173
QY 400 GTGCGTGGTGGC-----CTGGAGTTTGGTGTGGGCTCTTCATCTCCAC 444
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Db 174 IleAlaGlyGlyValGlyAsnGlnHisIleProGlyAspAsnSerIleTyrValThrLys 193
QY 445 CTCATCAAAAGGGGCTCAGGCAGACACGCTCGGG---CTCAGGTAGGGACGACGATCGTC 501
Db 194 IleIleGluGlyAlaAlaHisLysAspGlyArgLeuGlnIleGlyAspLysIleLeu 213
QY 502 CGGATCAATGGATATTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
Db 214 AlaValAsnSerValGlyLeuGluAspValMetHisGluAspAlaValAlaLeuLys 233
QY 562 ---ACCAAGAAACTGTGTCATCAAGTG-----AGACACATCGGCTGATCCCC 609
Db 234 AsnThrTyrAspValValTyrLeuLysValAlaLysProSerAsnAlaTyrLeuSerAsp 253
QY 610 GTCAAAAGCTCTCTCATGAGCCCTCACTTGG---CAGTATGTGTGATCAGTTTGTGTG 666
Db 254 SerTyrAlaProAspIleThrSerTyrSerGlnHisLeuAspAsnGluIleSer 273
QY 667 GAATCTGGGGCGTGGCAGGCGCTTGGC----- 696
Db 274 HisSer-----SerTyrLeuGlyThrAspTyrProThrAlaMetThrProThr 289
QY 697 -----TCCCTCGAAATCGGAA-----AACAG 720
Db 290 SerProArgTyrSerProValAlaLysAspLeuLeuGlyGluAspIleProArg 309
QY 721 GAGAAGAAGCTCTTCATCAGCCCTGCTAGGCTCCCGAGGCTTGGCTGCGACGATTTCCAGC 780
Db 310 GluProArgArgIleValIleHisArgGlySerThrGlyLeuGlyPheAsnIleValGly 329
QY 781 GSCCCCATCCAGAGCTGGCATCTTTATCAGCCATGTG-----AACTGCTGCTCC 831
Db 330 GlyGlu---AspGlyGluGlyIlePheIleSerPheIleLeuAlaGlyGlyProAlaAsp 348
QY 832 CTGCTCTGCTGAGTGGGATTGGAGTAGGGGACGATTTGTCGAGTCAATGCTGCTGAC 891
Db 349 LeuSerGlyGlu-----LeuArgLysGlyAspGlnIleLeuSerValAsnGlyValAsp 366
QY 892 TTCTCTAACTGGATCACAAGAGGCTGTAAATGTCTCAAAATAATGCGCAGCCTGACC 951
Db 367 LeuArgAsnAlaSerHisGluGlnAlaAlaIleAlaLeuLysAsnAla---GlyGlnThr 385
QY 952 ATCTCATTTAGTGTGACGCTGCGCGGAGCTGTTTCATCAGACACCGGGAGCGGTGGCA 1011
Db 386 ValThrIleIleAlaGln-----TyrLysProGluGluTyrSerArgPhe 400
QY 1012 GAGGCGGCGCAGCTGAGCTGCGGCGGAGGAGCTTCTCATCAGAGCGGCTG----- 1065
Db 401 GluAlaLysIleHisAspLeuArgGluGln-----LeuMetAsnSerSerLeuGlySer 418
QY 1066 -----GCGATGGAGTCCAAC----- 1080
Db 419 GlyThrAlaSerLeuArgSerAsnProLysArgGlyPheTyrIleArgAlaLeuPheAsp 438
QY 1080 ----- 1080
Db 439 TyrAspLysThrLysAspCysGlyPheLeuSerGlnAlaLeuSerPheHisPheGlyAsp 458
QY 1081 -----AGATCTCTCAGGAGCAGCAGGAGATGGAGCGGCAAGGAGAAAGAAATGGC 1134
Db 459 ValLeuHisValIleAspAlaSerAspGluGluTyrTrpGlnAlaArgValHisSer 478
QY 1135 CAGAAAGCAGCAGGAGGAAATCAGAGATACCGGAGGAGATGGAACAGATTTGTAGAGGAG 1194
Db 479 AspSerGluThrAsp-----AspIleGlyPheIleProSerLys 491
QY 1195 GAAGAGAAGTTTAAGAGCAATGGAA-----GAAGACTGGGGCTCA----- 1236
Db 492 ArgArgValGluArgArgGluTrpSerArgLeuLysAlaLysAspTrpGlySerSerSer 511
QY 1237 -----AAGAACAGCTACTCTTGGCTTAAACCTCACT---GCTGAGGTA 1278
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Db 310 GluProArgValIleValIleHisArgGlySerThrGlyTrpGlyPheAsnIleValGly 329  
 QY 781 GCGCCCATCCAGAGCGCTGCATCTTTATCAGCCATGTG-----AAACCTGCGCTCC 831  
 Db 330 GlyGlu---AspTyrGluGlyIlePheIleSerPheIleLeuAspGlyGlyProAlaAsp 348  
 QY 832 CTGTCTGCTGAGGTGGATGGAGATAGGGGACCATGTCGAGTCAATGCGCTCGAC 891  
 Db 349 LeuSerGlyGluGlu-----ArgTysGlyAspGlnIleLeuSerValPheGlyValAsp 366  
 QY 892 TTCTCTAACTGGATCACAAGAGGCTGTAAATGTGCTGAAAAATAGCGCGAGCTGACC 951  
 Db 367 LeuArgAsnAlaSerHisGlyGlnAlaIleAlaLeuIleYsAsnAlaHisGln---Thr 385  
 QY 952 ATCTCCATTGTAGCTCAGCTGCGCGGAGCTGTTTCATCAGACAGCGGAGCGCTGGCA 1011  
 Db 386 ValThrIleIleAlaGln-----TyrIleProGluGluTyrSerArgPhe 400  
 QY 1012 GAGCGCGCGAGGCTGAGCTGCAGCGGCGAGGAGCTTCTCATGCAGAGCGGCTGGCGATG 1071  
 Db 401 GluAlaLeuIleHisAspLeuArgGluGlnLeuMetMetSerSerLeuGlySerGlyThr 420  
 QY 1072 GAGTCCACAAGATCTCCAGGAGCAGCAGGAGATGGAGCGGCAAGAGGAGAAAGAAATT 1131  
 Db 421 AlaSerAsnArg-----SerAsnProIysArgGlyPhe 431  
 QY 1132 GCCCAGAGCGCAGCAGAGGAAATGAGATACCGGAAG----- 1170  
 Db 432 TyrGlnArgAlaLeuPheAspTyrAspLysThrArgAspCysGlyPheLeuSerGlnAla 451  
 QY 1170 ----- 1170  
 Db 452 LeuThrPheHisPheGlyAspValLeuHisValAlaSerAspGluTrpTrp 471  
 QY 1171 GAGATGGAACAGATTCTAGCAGGAGGAGAGAGT----- 1206  
 Db 472 GlnTrpArgArgValHisSerAspSerGluThrTyrAspIleGlyPheIleProSerLys 491  
 QY 1207 -----AAGAAGCAATGGGAA-----GAAGACTGGGGCTCA----- 1236  
 Db 492 ArgAlaValGluArgArgGluTrpSerArgLeuAspAlaLysAspTrpGlySerSer 511  
 QY 1237 -----AAGAAGCAAGTACTCTTGCTTAAACCATCACT---GCTGAGGTA 1278  
 Db 512 GlyGluGlnGlyArgGluAspSerValLeuSerPheGluThrValThrGlnMetGluVal 531  
 QY 1279 CACCCAGTACCCCTTCGCAAGCAAGATGTTCCGGAATATGAGGAAGGCTTTGACCC 1338  
 Db 532 HisGlyAlaArg-----Pro 536  
 QY 1339 CTACTCTATGTTTACCCAGCAGATCATGGGAAGGATGTCCGCGCTCTAGCATCAA 1398  
 Db 537 IleIleIleLeuGlyProHisLysAspArgAla----- 547  
 QY 1399 GAAGAGGAGATCTTAGACTGCGCTGGAAGCGGTGTGGACTCCCCCATTTGGGAAGT 1458  
 Db 548 AsnAspAspLeuIleGluPheProAspLys----- 558  
 QY 1459 GGTGCTTTCTGTGTATGAGCGGCGAGCTGCTGAGCGCATGGTGGCATTTGTGAAGG 1518  
 Db 559 -----PheGlySerCys-LysProHisThrThrArgProLys 571  
 QY 1519 GGACGAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTGGCTGAGGCTGA 1578  
 Db 571 gglu-----LeuGluIleAspGlyArg-----AspTyrHisPheMetSerSer 586  
 QY 1579 CGCTGCCCTGCAGAAAGCGCTTGAATCAGGCGGGGAGTGGATCGACCTTGTGGTCCCT 1638  
 Db 586 gGluLysMetGluLys----- 591  
 QY 1639 CTGCCCCCAGAGGATATGACATGAGCTGACCTTCTTGTCTGAGTCCAAAGGGGAAA 1698  
 Db 592 -----AspAsnGlnAlaHisLysPheIleGluAlaGlyArgTyrAs 605

QY 1699 CCAATTCACGCGTTAGGAAACAGT-----GAGCTCGGCGC 1734  
 Db 605 nSer---HisLeuTyrGlyThrSerSerGlnSerValArgGluValAlaGluGlnThrLy 624  
 QY 1735 CCACCTCGTGAACACAAAGCCCTCGGACAGCCTTGAGAGAGCCACATGACACACACAG 1794  
 Db 624 shiCysIleLeuAspValSerAlaValAlaValArgLeuGlnAlaHis----- 642  
 QY 1795 ATGGCATCTCTGGGACCTGAATCTATCACCCAGGAATCTCAAACTCTTGGCCCTGAA 1854  
 Db 643 -TrpHisProIleAlaIlePheIleArgProTyrSerLeuGluAsnValLeuGluIleAs 662  
 QY 1855 C-----CAGGGCCAGATAGGAACACAGCTCGGGCCACTTTTGAAG- 1895  
 Db 662 nAlaArgIleThrGluGluGln-AlaArgLysAspPheAspArgAlaThrLysLeuGluG 682  
 QY 1896 -----GCCAATGTGAGGAAAGGAGGAGCCAGCCGTTTGGG 1932  
 Db 682 InPhePheThrGluCysPheSerAlaIleValGlyCysPheSerPheGluGluIleTyrH 702  
 QY 1933 AGAAGATCTCAAGATC-----CAGACTCTCATCTCTTCTCTCTGG 1973  
 Db 702 ishivallysargValIleGluAspLeuSerIleProTyrIleTrp 717  
 RESULT 12  
 US-09-045-632-50  
 ; Sequence 50, Application US/09045632  
 ; Patent No. 6001575  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huginir, Richard L.  
 ; APPLICANT: Dong, Hualing  
 ; TITLE OF INVENTION: THERAPEUTIC USES OF GRIP AND  
 ; TITLE OF INVENTION: GRIP-RELATED MOLECULES  
 ; NUMBER OF SEQUENCES: 105  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 ; STREET: 130 Water Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/045,632  
 ; FILING DATE: 19-MAR-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/041,016  
 ; FILING DATE: 19-MAR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Corlees, Peter F.  
 ; REGISTRATION NUMBER: 33,860  
 ; REFERENCE/DOCKET NUMBER: 48147/1699-CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-523-3400  
 ; TELEFAX: 617-523-6440  
 ; INFORMATION FOR SEQ ID NO: 50:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1050 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-045-632-50  
 Alignment Scores: 4.7e-09 Length: 1050  
 Pred. No.: 206.50 Matches: 169  
 Score:

Percent Similarity:	35.22%	Conservative:	99
Best Local Similarity:	22.21%	Mismatches:	264
Query Match:	5.18%	Indels:	239
DB:	3	Gaps:	35
US-09-502-945-5 (1-2162) x US-09-045-632-50 (1-1050)			
QY	322	CAGCTGACCCCGCGCTCCAGGAGCTGAAGAGGTGGCTGCGACCGCTGACACCC	381
DB			
DB	77	GlnSerIleProGluGluPheArgGlyIleThrMetValGluLeuLeuLysArgGluGly	96
QY	382	GAAGGCTCGGCTCAGTGTGGCTGGCTCGAGTTTGGCTGGCTCTTCATCTCC	441
DB			
DB	97	SerThrLeuGlyLeuThrIleSerGlyIleThrAspLysAspGlyLysProArgValSer	116
QY	442	CACCTCATCAAGGGGT---CAGGACAGACGGCTCGGCTCCAGTAGGGACAGATC	498
DB			
DB	117	AsnLeuArgProGlyGlyLeuAlaAlaArgSerAspLeuLeuAsnValGlyAspTyrIle	136
QY	499	GTCGGATCAATGGATATTCATCTCTCTCTGTCACCATGAGAGGTCACTCACTCAT	558
DB			
DB	137	ArgSerValAsnGlyIleArgLeuThrArgLeuArgHisAspGluIleIleThrLeuLeu	156
QY	559	CGAACC-----	564
DB			
DB	157	LysAsnValGlyGluArgValValLeuGluValGluTyrGluLeuProProAlaPro	176
QY	565	-----AAGAACTGTGTCCATCAAAAGTG-----AGA	591
DB			
DB	177	GluAsnAsnProArgIleIleSerLysThrValAspValSerLeuTyrLysGluGlyAsn	196
QY	592	CACATCGGCTGATCCCGTGAAAGCTCTCTGATGAG-----CCCTC	636
DB			
DB	197	SerPheGlyPheValLeuArgGlyGlyAlaHisGluAspLeuHisLysSerArgProLeu	216
QY	637	ACTTGCAGTATGTG-----	651
DB			
DB	217	ValLeuThrTyrValArgProGlyGlyProAlaAsnArgGluGlySerLeuLysValGly	236
QY	652	GATCATTTGTGCGAATCTGGG-----	675
DB			
DB	237	AspArgLeuLeuSerIle**GlyIleProLeuHisGlyAlaSerHisAlaThrAlaIle	256
QY	676	-----GGCGTCGAGGCGCTGGCTCC	699
DB			
DB	257	AlaThrLeuGlnGlnCysSerHisGluAlaLeuPheGlnValGluTyrAspValAlaThr	276
QY	700	CCTGGAATCGGGAACCAAGGAGAGGTCTTCATCAGCTGTGTAGGCTCCCGAGGC	759
DB			
DB	277	ProAspThrValAlaAsnAlaSerGlyProLeuValValGluLeuAlaLysThrProGly	296
QY	760	-----CTTGGTGCAGCATTTCCAGCGCCCATCCAG---AAGCTGGCATCTTTATC	810
DB			
DB	297	SerAlaLeuGlyIleSerLeuThrThrGlySerHisArgAsnLysProAlaIleThrIle	316
QY	811	AGCCATGTAACCTGGCTCCCTGCTGCTGAGTGGGA---TTGGAGATAGGACACAG	867
DB			
DB	317	AspArgIleLysProAlaSerValValAspLysAsnGlyAlaLeuHisAlaGlyGluHis	336
QY	868	ATTGTCAAGATCAATGGCTCGACTTCTCTAACCCTGGATCACAAAGAGGCTGTAAATGTG	927
DB			
DB	337	IleLeuAlaIleAspGlyThrSerThrGluHisCysSerLeuValGluAlaThrLysLeu	356
QY	928	CTGAAAT---AGCCGAGCTGACCATCTCCATTTGATGTCGA-----GCTGGCCGG	978
DB			
DB	357	LeuAlaSerValThrGluLysValArgLeuGluIleLeuProAlaProGlnSerArgArg	376
QY	979	GAGCTGTTATGACACACCGGAGCGGTGGCGAGCGCGCGAGGTG-----	1027
DB			
DB	377	ProLeuLysProProGluAlaValArgIle-GlnArgSerGluGlnLeuHisIleTrpAs	396
QY	1028	-----AGCTGC---AGCGCAGGAGCTTCTCATGTCAGAAAGCGGCTGGCGATG	1071
DB			

DB	396	pProCysValProSerCysHisSerProArgProSerHisCysArgAlaPro---Thr	415
QY	1072	GAGTCCA-----ACAGATCTCCAGGAGCAGCAGGAGATGAGCGGC-----	1114
DB			
DB	415	pAlaProGlyGlyGlnAspGlnSerArgSerValSerSerThrProPheSerSerProTh	435
QY	1115	-----AAAGGAGAAAGAAATTTCCAGAGGAGCAGCAGAGGAA	1152
DB			
DB	435	rMetAsnProAlaPheProCysAlaAsnAlaSerThrLeuProArgGlyProMetSerPr	455
QY	1153	AATGAGATACCGGAAGAGAGATGGAACAGATTGTAGAGHAGGAAGAGA-----	1201
DB			
DB	455	oArgThrThrAlaGlyArgArgGln-----ArgArgLysGluHisArgSerSe	472
QY	1202	---AGTTTAAAGCAATGGGAAGACACTGGGCTCAAGGAACAGACTACTCTTGCT	1257
DB			
DB	472	rLeuSerLeuAlaSerSerThrValGlyProGlyGlyGln-----	485
QY	1258	AAAACCATCACTGCTGAGGTACACCCAGTACCCCTTCGCVAGCCAAAGTGATTTCCG	1317
DB			
DB	486	-----IleValHisThrGlu-----	490
QY	1318	ATATGAGGAGCTTTTGACCCCTACTCTATGTTCACCCAGAGCAGATCATGGGAAGA	1377
DB			
DB	491	-----ThrThrGluValValLeuCysGlyAs	499
QY	1378	TGTCGGCTCTACGCATCAAGAGGAGGATCCTTAGA-CTGGCCCTGGAGGCGGTGT	1437
DB			
DB	499	p-----ProLeuSerGlyPheGlyLeuGlnLeuGlnGlyIle	512
QY	1438	G-----GACTCCCACTTTGGGAAGGTGTGTCTTCTGCTGTGTATGA	1479
DB			
DB	512	ePheAlaThrGluThrLeuSerSerPro-----ProLeuValArgPheIleGluPr	529
QY	1480	GGGGGAGCTGCTGAGCGGCATGTGGCATTTGTAAAGGAGAGCAGATCATGGCAATCA	1539
DB			
DB	529	oAspSerProAlaGluArgCysGlyLeuLeuGlnValGlyAspArgValLeuAlaIleAs	549
QY	1540	CGGCAAGATTGTGACAGACTACACCTGCTGCTGAGCT-----GAGCTGC	1584
DB			
DB	549	nglyIleAlaThrGluAspGlyThrMetGluAlaAlaGlnLeuLeuArgAspAlaAl	569
QY	1585	CCTGAGAAAGGCTCGAATCAGGCGGAGCTGAGATCGA-CTTGTGTGTTGCGCTGCTCC	1644
DB			
DB	569	aleuAlaArgLysIleValLeuGluIleGluPhe---AspValAlaGluSerValIlePr	588
QY	1645	C-----CCAAAGAGTAGTACGATGAGCTGACCTCTCTT	1677
DB			
DB	588	oSerSerGlyThrPheHisValLysLeuProLysArgArgGlyValGluLeuGlyIleTh	608
QY	1678	GCTGAAGTCC-----AAAAGGGAAACCAATTCACGCGTTAGGAAACAGTGAGCT	1728
DB			
DB	608	rIleSerSerAlaSerArgLysArgGly-----	617
QY	1729	CGGCGCCACCTCGTGAACACACAAAGCCTCGGACCGCTTGAGAGAGGCCACATGACAC	1788
DB			
DB	618	-GluProLeuIleIle-----SerAspIleLysLysGlySerValAlaAla	632
QY	1789	CACC-----AGATGGCATCTTGGGACCTGAATCTATCACCAGGAATCTCAAACTC--	1840
DB			
DB	632	sArgThrGlyThrLeuGluProGlyAspLysLeuAlaIleAspAsnIleArgLeuAs	652
QY	1841	-----CTTTGGGC-----CTCAACCCAGG	1860
DB			
DB	652	pHisCysProMetGluTyrAlaValGlnIleLeuProGlnCysGluAspLeuValLysLe	672
QY	1861	CCAGATAAGGAACAGCTCGGCGCCACTTTTTCAGGCGCAATCTGGAGGA-----	1909
DB			
DB	672	uLysIleArgLysAspGluAspAsnSerAspGluGlnGluSerSerGlyAlaValSerTy	692
QY	1910	-----AAGGGAGCAGCCGCGTTTGGGA-----GAAGA	1938
DB			
DB	692	rThrValGluLeuLysArgTyrGlyGlyProLeuGlyIleThrIleSerGlyThrGluGl	712





Db 1344 o-----GlyAspIlePheGluValGluLeuAlaLysAsnAspAsnSerLeuGlyIleSe 1362  
Qy 1423 CTGGAAGCGGTGTGAGCTCCCCATT-----GGGAAGTGGTGGTTCTGCTGTGTA 1476  
Db 1362 rValThrGlyGlyValAsnThrSerValArgHisGlyGlyIleTyrValLysAlaVal11 1382  
Qy 1477 TGAGCGGAGGTGCTGAGCGGCATGTCGGCATTTGTAAAGGGGACGAGATCATGGCAAT 1536  
Db 1382 eProGlnGlyAlaAlaGluSerAspGlyArgIleHisLysGlyAspArgValLeuAlaVa 1402  
Qy 1537 CAACGCAAGATTGTACAGACTACACCTGCTGAGCTGAGCTGACGTCGCCCTG----- 1588  
Db 1402 laeGlyValSerLeuGluGlyAlaThrHisLysGlnAlaValGluThrLeuArgAsnTh 1422  
Qy 1588 ----- 1588  
Db 1422 rGlyGlnValValHisLeuLeuGluLysGlyGlnSerProThrSerLysGluHisVa 1442  
Qy 1589 -----CAGAAAGCGCTCGAATCAGCGGGGAGCATG 1617  
Db 1442 lProValThrProGlnCysThrLeuSerAspGlnAsnAlaGlnGlyGlnGlyProGluLy 1462  
Qy 1618 GATCGACCTGTGGTGGTGGCTGCGTCCCGCCCAAGAGGATGAC-----GATGAGCT 1668  
Db 1462 sValLysLysThrThrGlnVal-----LysAspTyrSerPheValThrGluGluAs 1479  
Qy 1669 GACCTTC-----TTGCTGAGTCCAAAGGGGAAACCAATTCACGCGTTAGGAAA 1719  
Db 1479 nThrPheGluValLysLeuPheLysAsnSerSerGlyLeuGlyPheSerPheSerArgGl 1499  
Qy 1720 CAGTGAGCTCCGCGCCCGCCACCTCGTGAAC 1747  
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RESULT 14

US-09-566-076-12  
; Sequence 12, Application US/09566076  
; Patent No. 6475775  
; GENERAL INFORMATION:  
; APPLICANT: Sarab, Jan  
; APPLICANT: Franzn, Petra  
; APPLICANT: Aspenstrm, Pontus  
; APPLICANT: Hellman, Ulf  
; APPLICANT: Gonez, Leonel Jorge  
; APPLICANT: Haldin, Carl-Henrik  
; TITLE OF INVENTION: PARQ, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1  
; FILE REFERENCE: L0461/7030  
; CURRENT APPLICATION NUMBER: US/09/566,076  
; EARLIER FILING DATE:  
; EARLIER APPLICATION NUMBER: 09/080,855  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 2466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-566-076-12

Alignment Scores:  
Pred. No.: 1,15e-08 Length: 2466  
Score: 204.50 Matches: 143  
Percent Similarity: 36.35% Conservative: 94  
Best Local Similarity: 21.93% Mismatches: 214  
Query Match: 5.13% Indels: 201  
DB: 4 Gaps: 29

US-09-502-945-5 (1-2162) x US-09-566-076-12 (1-2466)

Qy 1 CTGGCGCGGTGCGGTGCGGTCTTT----- 27  
Db 991 ProProGlnThrValAlaGluLeuValGlyLysProSerHisGlnMetSerArgSer 1010

Qy 28 ---TCCAGTCTCTGCGACCGGGCACCCGAAGAAACGGGTCGTGCAACGACCCAGCTGGA 84  
Db 1011 AspAlaGluSerLeuAlaGlyValThrLysLeuAsnAsnSerLysSerValAla----- 1028  
Qy 85 CTGGCCCGCATGAGACCGAAAGTGGCCGAGAAATTCGGCATAAGGTGATTTCTG 144  
Db 1029 -----SerLeuAsnArgSerProGluArgArg-----LysHisGluSerAspSer 1044  
Qy 145 ATTGAATAATGTCAGAGAAGGACTATCTCTATGATGTGTCGGAATGTACCAACAGACC 204  
Db 1045 SerIleGluAspProGlyGlnAlaTyrValLeuAspValLeu-----HisLysArg 1061  
Qy 205 ATGAGCTGGCGCTGCTCTGCGAGACCTGGAAGCTGGTCAATCAATGAACCCAGCGCTG 264  
Db 1062 TrpSer-----IleValSerSerProGluArg--- 1070  
Qy 265 CCTCTGTTTGTATGTCATTCGGCGGTGATCCACATGAGACACAGGTGGAATATGATCAG 324  
Db 1071 -----GluIleThrLeuValAsnLeuLysLysAspAlaLysTyr----- 1083  
Qy 325 CTGACCCCGCGCGCTCCAGGAAGCTGGAAGGAGTGGCTTGGACCGTCTGCACCCCGAA 384  
Db 1083 ----- 1083  
Qy 385 GGCTCGCGCTGAGTGTGCTGCTGGCTGGCTGGAGTTTGGC-----TGTGGGCTTTC 435  
Db 1084 GlyLeuGlyPheGlnIleIleGlyGlyGlyLysMetGlyArgLeuAspLeuGlyIlePhe 1103  
Qy 436 ATCTCCACCTCATCAAGCGCGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492  
Db 1104 IleSerSerValAlaProGlyGlyProAlaAspPheHis3LysLeuLysProGlyAsp 1123  
Qy 493 GAGATCGTCGGATCAATGGATATTCATCTCTCTGTACCCATGAGGAGGAGGAGGAGGAG 552  
Db 1124 ArgLeuIleSerValAsnSerValSerLeuGluGlyValSerHisHisAlaIleGlu 1143  
Qy 553 CTCATTGCAACCAAGAAACCTGTGTCCATCAAGTGAGACACATCGGCTGATCCCCGTG 612  
Db 1144 IleLeu----- 1145  
Qy 613 AAAAGCTCTCTGTATGAGCCCTCACTTGGCAGTATGTGATGATGTTGTGTCGGAATCT 672  
Db 1146 GlnAsnAlaProGluAsp-----ValThrLeuValIleSerGlnPro 1159  
Qy 673 GGGGCGTGGCAGGAGCGCTGGGCTCCCTCGAAATCGG3AAAAACAAGGAGGAAGAGTC 732  
Db 1160 -----LysGluLys----- 1162  
Qy 733 TTCATCAGCTGTTAGGCTCCCGAGGCTTGGCTGCAGCATTTCCAGCGCGCCCATCCAG 792  
Db 1163 ---IleSer-----LysValProSerThrProValHis 1172  
Qy 793 AAGCTGGCATCTTATCATGCCATGTGAACCTGGCTCCCTGCTGCTGCTGAGTGGGATG 852  
Db 1173 LeuThrAsnGluMetLysAsnTyrMetLysSerSer----- 1185  
Qy 853 GAGATAGGGGACCATGTTCTCGAAGTCAATGCGCTGCTCTTAACCTGGATCAACAAG 912  
Db 1186 -----TyrMetGlnAspSerAlaIleAspSerSerLysAspHisHis 1200  
Qy 913 GAGGCTGTAATGTCTGAAAAAATAGCGCGACCTGACCATCTCCATTTAGCTGCAGCT 972  
Db 1201 TrpSerArgGlyThrLeu-----ArgHisIleSerGluAsnSerPheGlyProSer 1217  
Qy 973 GGC-----CGGAGCTGTTATGACAGACCGGGAGCGCTGGCAGAGCGCGGCGGCGGT 1026  
Db 1218 GlyGlyLeuArgGluGlySerLeuSerSerGlnAspSerArgThrGluSerAlaSerLe 1237  
Qy 1027 GAGCTGCAGC-----GGCAGGAGCTTCTCATGACAGAACCGC-----TGGCGATG 1071  
Db 1237 userGlnSerGlnValAsnGlyPhePheAlaSerHisLeuGlyAspGlnThrTrpGlnG 1257  
Qy 1072 GAGTCCCAACAGATCTCTCCAGGAGCAGGAGAGATGGACCGGCAAGAGGAGAAAGAAATT 1131

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Db 1257 user-GlnHisGlySerProSerProSerValIleSerLysAlaThrGluLysGluThrP 1277
QY 1132 GCCAGAGCCAGCAGAGGAAATGAGATACCGGAA---GGAGATGGAACAGATTGT- 1187
Db 1277 heThrAspSerAsnGlnSerLysThrLysLysProGlyLysSerAspValThrAspTyrS 1297
QY 1188 -----AGAGGAGGAGAGAGTATTAGAGCAATGGGAGAGACAGCTGGGGCTCAAGGAA 1242
Db 1297 erAspArgGlyAspSerAspMetAspGluAla-----T 1308
QY 1243 CAGCTACTCTTGCTAAACCATCACTGCTGAGGTACACCCAGTACCCCTTGCAAGCCA 1302
Db 1308 hrTyrSerSerGlnAspHisGln-----ThrProLysGlnGluSerSerS 1325
QY 1303 AAGTGATTTCCGGAATATATGAGGAAGCTTTGACCCCTACTCTATCTTCCACCCAGAGCA 1362
Db 1325 erValAsnThrSerAsn---LysMetAsnPhelysThrPheSerSerProProLysPr 1344
QY 1363 GATCATGGGAGGATGTCGGGCTCTACGATCAAGAGGAGGATCTCTAGACCTGGC 1422
Db 1344 o-----GlyAspIlePheGluValGluLeuAlaLysAsnAspAsnSerLeuGlyIleSe 1362
QY 1423 CTGGAAGGGGTGCTGACTCCCCATT-----GGAGGTGGTCTGTTCTCTGTGTA 1476
Db 1362 rValThrGlyGlyValAsnThrSerValArgHisGlyGlyIleTyrValLysAlaValI 1382
QY 1477 TGAGCGGGAGCTGCTGAGCGGCATGTGTCATTGTGAAGGGGAGGAGATCATGGCAAT 1536
Db 1382 eProGlnGlyAlaAlaGluSerAspGlyArgIleHisLysGlyAspArgValleuAlaVa 1402
QY 1537 CAACGCAAGATGTGACAGACTACACCTGCTGCTGAGGTGAGCTGAGCTGCCCTG----- 1588
Db 1402 laenGlyValSerLeuGlyAlaThrHisLysGlnAlaValGluThrLeuArgAsnTh 1422
QY 1588 ----- 1588
Db 1422 rGlyGlnValValHisLeuLeuGluLysGlyGlnSerProThrSerLysGluHisVa 1442
QY 1589 -----CAGAAGCGCTGGAATCAGGCGGGGAGCTG 1617
Db 1442 lProValThrProGlnCysThrLeuSerAspGlnAsnAlaGlnGlyGlnGlyProGluLy 1462
QY 1618 GATCGACCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1668
Db 1462 sValLysLysThrThrGlnVal-----LysAspTyrSerPheValThrGluGluAs 1479
QY 1669 GACCTTC-----TTGCTGAGTCCAAAGGGGAAACCAATTCACGCGTTAGGAA 1719
Db 1479 nThrPheGluValLysLeuPheLysAsnSerSerGlyLeuGlyPheSerPheSerArgGl 1499
QY 1720 CAGTGAGCTCCGGCCCGCCACCTCGTGAAC 1747
Db 1499 uAspAsnLeuIleProGluGlnIleAsn 1508

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## RESULT 15

PCT-US94-09943-2

; Sequence 2, Application PC/TUS9409943

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; NUMBER OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY, MICHAEL J.
; REGISTRATION NUMBER: P-38,349
; REFERENCE/DOCKET NUMBER: LO461/7000WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZBKIL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-09943-2

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Alignment Scores:
Pred. No.: 1,158-08 Length: 2466
Score: 204.50 Matches: 143
Percent Similarity: 36.35% Conservative: 94
Best Local Similarity: 21.93% Mismatches: 214
Query Match: 5.13% Indels: 201
DB: 5 Gaps: 29

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US-09-502-945-5 (1-2162) x PCT-US94-09943-2 (1-2466)

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QY 1 CTGCGCCCGTCCGGTCCGGCTCTT----- 27
Db 991 ProProGlnThrValAlaGluLeuValGlyLysProSerHisGlnMetSerArgSer 1010
QY 28 ---TCAGGTCTCGGAGCCGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84
Db 1011 AspAlaGluSerLeuAlaGlyValThrLysLeuAsnAsnSerLysSerValAla----- 1028
QY 85 CTGCGCCAGCATCGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 144
Db 1029 -----SerLeuAsnArgSerProGluArgArg---LysHisGluSerAspSerSer 1044
QY 145 ATTGAAATGATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 204
Db 1045 SerIleGluAspProGlyGlnAlaTyrValLeuAspValLeu-----HisLysArg 1061
QY 205 ATGAGCGTGGCGGTGCTGCTGGGAGACCTGAGAGCTGATCATCAATGAACCCAGCCGCTCTG 264
Db 1062 TrpSer-----IleValSerSerProGluArg--- 1070
QY 265 CCTCTGTTTGATGCCATTCGGCGGTGATCCACCTGAAGCAGCAGGAGGAGGAGGAGGAGGAGGAG 324
Db 1071 -----GluIleThrLeuValAsnLeuLysLysAspAlaLysTyr----- 1083
QY 325 CTGACCCCGCGCGCTCCAGGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 384
Db 1083 ----- 1083
QY 385 GGCCTCGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
Db 1084 GlyLeuGlyPheGlnIleIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1103
QY 436 ATCTCCACCTCATCAAGGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
Db 1104 IleSerSerValAlaProGlyGlyProAlaAspPheHisGlyCysLeuLysProGlyAsp 1123

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